

# STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number: 123041

TO: Georgia L Helmer

Location: REM-2C15&2C18

Art Unit: 1638

Wednesday, June 02, 2004

Case Serial Number: 10/015637

From: Mary Jane Ruhl

**Location: Biotech-Chem Library** 

Remsen 1-B55

Phone: 571-272-2524

maryjane.ruhl@uspto.gov

#### Search Notes

Examiner Helmer, ...

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl Technical Information Specialist STIC CM-1, Rm. 6-A-06 605-1155



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Perfect score:
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REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX463281	RESULT 1
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/mol_type="unassigned DNA"
/db_xref="taxon:3885"
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Eukaryota; Vagnoliophyta; eudicotyledons; core eudicots;
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/mol_type="unassigned DNA"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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/mol_type="unassigned DNA"
/db_xref="taxon:3885"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                             Submitted (13-AUG-1998) Goossens A., Universiteit Gent, Laboratorium Genetika, K.L.Ledeganckstraat 35, Gent, Belgium, On Aug 25, 1998 this sequence version replaced gi:929816.
                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01-AUG-1995) Goossens A., Universiteit Gent, Laboratorium Genetika, K.L.Ledeganckstraat 35, Gent, Belgium,
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Nucleotide sequence of an arcelin5-I
Phaseolus vulgaris
plant Physiol. 109, 722-722 (1995)
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                  /tissue_type="leaf"
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                                                           haplotype="arc5"
                                                                               /db_xref="taxon:3885"
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         AATAATTGTAATTAGGTTTTCTAGTCATGAGCACCACTCAGAGACAAGATTTCAAGAAAA
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/product="arcelin 5a"
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/protein id="cas0585.1"
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/db_xref="GI:3451282"
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/db_xref="GOI:042
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2726. .2731
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1792. .1797
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2722. .2727
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1835. .2620
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|822. .2754
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5 2 AX4632B2 1122 bp DNA linear PAT 15-JUL-2002 ION Sequence 2 from Patent WO0250295. DN AX463282	1141 TTAATGCA 1148         1814 TTAATGCA 1821	1081 AAGAAAAAGTTGGAAAACATTTTGCATTTGTTGTATAATACAGAACAGAGTGATGG 1140	1 CETGGATGCATTGCCATCGTTGTTTAATTATTGTTAATTTGCAGTTGCAATAATAAATGA 10	30 mm 30	AAACCG	, <sub>1</sub> , <sub>9</sub>	H-1 H-	21 GCTGCCACCTCAGCTCCCTCCTCCACACATGTCTCATGTCTACTTTCGACTTTTCGACTTTTCTATCTA	661 AAAAAGGGAAATCAAATTAGAATTTTGATTCCCCACATGACACCAACTCACCATGCAC 720			AGTTTATAGAAATACAAATATTTAAAAAATATAATTTTAAAAAAACATTCTAAAGTCATT	421 GTTATACATATATTTTTGTAAAAACTTAGAGTTTTTCAAAACATTCTAATACATGATTAG 480 	4.	974 AAAAAAAGTACACGAGAAACACAATAAACCCCACTAGCGTCAGGTATCATAAGGATGA 1033 361 AATGTTTTGATATCATTAAATATAACACACACAAAAATACATCTAATTATAACAATATAT 420	10	241 CAATTTTGTTAAACATCTTATTAGAAACTTTTAGTTAAGTCTTGAAGTTAGAATTAAACA 300	854 AATAATTGTAATTAGGTTTTCTAGTCATGAGCACCACTCAGAGACAAGATTCCAAGAAAA 913
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663 661 723	603 601	543 541	483 481	423	363 361	Оу 303 Оъ 301	243 241	183 181	123 121	63 61	<b>μ</b> ω	11.	RIGIN	RENESSEN			NISM	
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Phaseolus vulgaris
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/mol_type="unassigned DNA"
/db_xref="taxon:3885"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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        AGTAAAAAGAATAAGAATAAACTAGTGAATATA-
                        CTCACACCGGTGAAATCATTTACTCGTAGTATAGTACCGTGTCATAATAGTTCACAACAC
                                                                         CTCACACCTGTGTGATCATTTAGTCAT-GTATGTAGTACAATCATTGTAGTTCACAACAG
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llarity 85.7%;
Conservative
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1. .1872
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Pred. No. 7.8e-117;
D; Mismatches 90;
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arcelin; lectin-like seed protein.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magmoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Phaseolus vulgaris
M68913
                                                                                                                                                                                                              Original source text: Phaseolus young plant leaf DNA.
                                                                                                                                                                                                                                      Anthony, J.L., Vonder Haar, R.A. and Hall, T.C. Nuclectide sequence of a genomic clone encoding lectin-like seed protein from Phaseolus Plant Physiol. 97, 839-840 (1991)
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3361. 337
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/tissue_lib="Lambda Zap I
                                                              /gene="arc"
3332. .3338
3361. .3364
/gene="arc"
/note="cap r
3375. .4172
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Phaseolus vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                             Direct Submission
Submitted (07-OCT-1999) Embrapa/Cenargen,
WS Norte, Brasilia, DF 70770-900, Brazil
Location/Qualifiers
                                                                                                                                                                          1 (bases 1 to 2288)
Gerhardt, I.R. and Grossi de Sa, M.F.
Molecular characterization of a new
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ATESCNFGHNNGEKAEVRITYDSPKNDLRVSLLYPSSEEKCVETVNSTTVPLEKEVEDWVS
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                                                                                                                                                                                                                                                                         1 (bases 1 to 1768)

1 (bases 1 to 1768)

1 (voelker, T.A., Staswick, P. and Chrispeels, M.J.

1 Molecular analysis of two phytohemagglutinin genes and their

1 expression in Phaseolus vulgaris cv. Pinto, a lectin-deficient

1 cultivar of the bean

1 EMBO J. 5, 3075-3082 (1986)

1 See also < X04659 > for Pélec2 gene.

1 Several inverted repeats are described in the 5' upstream region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pdlecl gene, phytohemagglutinin; pseudogene.

Phaseolus vulgaris

Phaseolus vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; Fabaceae; Papilionoideae; Phaseoleae;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
           the PHA gene.

None of the 3 possible reading frames allow the translation of its message into a complete PHA polypeptide. The PHA translational start codon (pos. 708-710) starts a RF which codes for a truncated 50AA polypeptide with a N-terminal sequence completely identical to the dlec1 gene product, but is out of register after 10 codons due to a single bp deletion (pos. 739/740).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phaseolus.
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603. .1385
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/clone="pIG53"
/tissue_type="leaf"
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ocation/Qualifiers
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cv.Pinto pseudogene
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source

/organism="Phaseolus vulgaris" /mol\_type="genomic DNA" /strain="Pinto UII11"

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                                                    PFAVAR23A 22243 bp DNA linear INV 14-81 Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's.
L40609.1 GI:886376
variant-specific surface protein.
Plasmodium falciparum (malaria parasite P. falciparum)
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                                                                                                                                                       TAATGCA 696
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/tissue_type="young leaves
665...670
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shift mutation)"
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/translation="MASSNLLSLALSLCFSPTQTQPAKPSSASIGSTKPTLSSKAMPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAA28363.1"
/db_xref="GI:21021"
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REFERENCE
AUTHORS
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PfYED9) b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Su,X.Z., Heatwole V.M., Wertheimer,S.P., Guinet,F., Herrfeldt,J.A., Peterson,D.S., Ravetch,J.A. and Wellems,T.E.

The large diverse gene family var encodes proteins involved in cytoadherence and antigenic variation of Plasmodium falciparum-infected erythrocytes (cell 82 (1), 89-100 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell 82
95330813
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 22243)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               606788
blood stage DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source text: Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="FCR3"
/dh v~re"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="blood stage"
427._.10322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:5833"
/clone="PfYED9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="var-3"
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                                                                                                                                                                                                                                                                                                                                                                                                                        protein_id="AAA75397.1"
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SLEXYRGOYOLNIS DIVINI CTELARS PADED I VBGRIDLY TERMILADIVCEAAKER AS
FROM TOGTCOTT THE TOTAL THE TOT VWDI IYDBYLKRKENELFGTNHYKQTSIHSVAKPARDDPIHNQLELFHKWLDRHRDMCEKLK MHHERLAKLKEEWENETHSGNTHPSDSNKTLNTOVSIQIHMONPKPINUETINDTILD DLDINNEPYYDVQDDIYYDVNDHDTSTVDSNAMDVPSKVQIEMDVNTKLVKEKYPIRD IQADGI PSSKI TDNEWNTLKDEFISQYLQSEQPNDVPNDYTSGNSSTNTNITTTSRHN VEEKPFIMSI HDRNLYTGEE INYNVMVNTHDDI PINRDNNVYSGI DLINDALNDYD LEBENPVEAPNICPKVEBPEPVVEEEKCDLABAPSKESSTEENSGEGSNSEQNPRSKP EEBPPPPTSSETDTPPPAPPTIQPSQADQPTNSISDILSSTIPPGIAIALISIVTLFL KKKTKSSUDLLRULNIPKGEYGNPTLKSSNRYIPYASDRYKGKTYIYMEGDSDSGHYY EDTTDVTSSESEYEELDINDIYVPGSPKYKTLIEVVLEPSGNNTTASGKNTPSDTQND 8218. /translation="myloraaggggdgidkrsakhlldsigkkvydkyhgdalopsng klkgtlslaifekapegkotsedpcdlaheyhttvtsgydkenpckdrpevrfsyteg /gene="var-3" 9093. .>10322 note="specific to blood stage; putative" (codon\_start=1 oin(11749. .18339,19338. .20741) | gene="var-2" 1749. .20741 'gene="var-3" 'number=2 /gene="var-3" protein\_id="AAA75398.1" /db\_xref=\*GI:886378" product="variant-specific surface protein" gene="var-2" .9092

ACCESSION VERSION KEYWORDS

glycoprotein;

X02408.1

GI:20985

haemagglutinin; lectin; phytohemagglutinin; signal

DEFINITION

pvDLEC1 1395 bp DNA linear F Phaseolus vulgaris dlec1 gene for phytohemagglutinin (erythroagglutinating phytohemagglutinin).

PLN 30-MAR-1995 1 (PHA-E)

SOURCE

ORGANISM

peptide.
Phaseolus vulgaris
Phaseolus vulgaris
Phaseolus vulgaris
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

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                                                                  ТСАСЛАСАGАGТАЛААТАЛАТАЛАБСАТАЛАСТАGGGAATATATATA 644
                                                                                         AGAGTTTATAGAAATACAAATATTTAAAAATATATTTAAAAAAACATTCTAAAGTCA
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18340..1937
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19338..>20738
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DB 8; Length 1395;  -08; 56; Indels 48; Gaps 5;	9.4%; Score 108.4; D larity 69.8%; Pred. No. 7.2e- Conservative 0; Mismatches	Query Match Best Local Simila Matches 240; Co
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ing phytohemagglutinin (aa	duct="erythroagglutinat 4)"	١٢
21 to -1) "	e="signal peptide (aa - 1199	
ILSMSFASKLSDGTISBALNLANFALMQII.	KSVLPEWVIVGFTATTGITKGNVETNDI 375437	sig_peptide
VSSKOQLALIVVNINGEPTIJSSLGRAFYSAPTQIWDNTTGAVAASPTSFTFNIDVPNN VSSKOQLALIVVNINGEPTIJSSLGRAFYSAPTQIWDNTTGAVAASPTSFTFNIDVPNN SGPADGLAFVLLPVGSQPKDKGGLLGLFNNYKYDSNAHTVAVBFDTLYNVHWDPKPRH IGIDVNSIKSIKTTTWDFVKGENAEVLITYDSSTKLLVASLVYPSLKTSFIVDTUL	VSSKQQLRLTINVUDNGEPTISSLGRAFY; VSSKQQLRLTINVUDNGEPTISSLGRAFY; SGPADGLAFVLLPVGSQPKDKGGLLGLF IGIDVNSIKSIKTITWDFVKGENAEVLIT	
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	/db_xref="GI:758251"	
ing phytohemaggiutinin"	<pre>/product="erythroagglutinati) /protein_id="CAA26256.1"</pre>	
	3751202 /codon_start=1	CDS
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	/note="cap region"	- 1
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	ganism="Phaseolus vulgari l_type="genomic DNA" _xref="taxon:3885"	(
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vulgaris phytohemagglutinin genes	1395) d Donaldson,D.D. n of two Phaseolus	REFERENCE 1 (bases 1 to AUTHORS Hoffman, L.M. an TITLE Characterization

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                                                                                                                                                                                                                                                                               Two tandem polyadenylation signals are present at positions 1294-1299 and 1299-1304. Direct and inverted repeats in the form of alternating pyrimidine and purine residues are located at positions 10-29 and 74-93, and an two inverted repeats were found at positions 923-930 and 949-956.

Draft entry and sequence [1] in computer-readable form were kindly provided by L.M. Hoffman (07-0CT-1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 1395)
Hoffman, L.M. and Donaldson, D.D.
Characterization of two Phaseolus vulgaris phytohemagglutinin closely linked on the chromosome
EMBO J. 4 (4), 883-889 (1985)
85257505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phaseolus vulgaris
Phaseolus vulgaris
Phaseolus vulgaris
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Bukaryota, Viridiplantae, eudicotyledons, core eudicots;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
rosids, eurosids I, Fabales, Pabaceae, Papilionoideae, Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHYDLECA 1441 bp DNA linear PIN 27-APR-1:
P.vulgaris phytohemagglutinin gene encoding erythroagglutinating phytohemagglutinin (PHA-E), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1441)
Hoffman, L.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Original source text: P.vulgaris cv. Tendergreen DNA, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1985)
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375, ,1202
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RS Mizry, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angilano, D., Anjelano, D., Anyagi, A., Ayodeji, M., Baca, B., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Blaiwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Brant, N., Buhay, C., Burch, P., Burrell, K., Calderon, B., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederith, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Durn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Faraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, B., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, B., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Hernandez, R., Hines, S., Hadun, S. L., Hodgson, A., Hogues, M., Hernandez, R., Hines, S., Hadun, S. L., Hodgson, R., Johnson, R., Li, Z., Liu, J., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1105 CATTTGTTGTTGTATAAATAGAGAAGAGAGTGATGGTTAATGCA 1148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 CAGTTGTTGTATAAATAGAGAAGAGAGTGATGGTTAATGCA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 ATGTATTTGATGACGTGTATGCATTGCCATCGTTGCTTAATTGTTATTTCTATATTCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      852 GCATGCATGCTGCCACCTCAGCTCCCACCTCTTCTCATTATGAGCCTACTGGCCATGCA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC111404 246611 bp I
Rattus norvegicus clone CH230-61K4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC111404.5 GI:30579008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCATGCATGCGGCCACCTCAGCTCCCTCCTCTTCACCCGTGTTTTCCAATGCTACGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCATGCACGCTGCCACCACAGCTTTCTCCTCTTTTCACTATGACACGACTGGCCATGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----TTTGATGACGTGGATGCATTGCCATCGTTGTTTAAT------AATTGTTA 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 246611)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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upstream of SphI site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438. .1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="phytohemagglutinin signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSVLPEWVIVGFTATTGITKGNVETNDILSWSFASKLSDGTTSEALNLANFALNQIL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9,48;
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Pred. No. 7.2e-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA linear HTG 13-MAY-2003
, WORKING DRAFT SEQUENCE, 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48
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Lorenuhewall, Louleged, H., Lozado, R.J., L., X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, B.,
Mangum, B., Mapua, P., Martin, R., Martin, R., Martinez, B.,
Minosavijevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
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Nankervis, C., Neal, D., Newton, N., Pal, S., Parks, K.,
Pasternak, S., Poindexter, A., Popovic, D., Primus, E., Pul, -L.,
Plopper, P., Poindexter, A., Popovic, D., Primus, E., Pul, -L.,
Pluzzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,
Sanders, W., Savery, G., Scheter, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Shetty, J., Shatsman, D., Waldron, L., Rose, J.,
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
Wang, O., Wang, S., Warren, J., Warren, R., Weil, X., White, F.,
William, R., Wilson, R., Willey, R., Wooden, H., Worley, K.,
Wright, D., Wang, J., Zhou, J., Zhou, S., Dunn, D., Von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
Direct Submission
                                                                                          Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77031), USA
On May 13, 2003 this sequence version replaced gi:24819049.
On May 13, 2003 this sequence version replaced gi:24819049.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold') within each contig-scaffold, assembly (a 'contig-scaffold') within each contig-scaffold, assembly (a 'contig-scaffold') within each contig-scaffold by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 246611)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Worley, K. C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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----- Genome Center
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/denbank\_draft\_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 4 contigs. The true order of the pieces

Assembly program: Atlas 3.0;
Consensus quality: 217670 bases at least Q40
Consensus quality: 219537 bases at least Q30
Consensus quality: 220430 bases at least Q20
Estimated insert size: 231456; sum-of-contigs esti
Quality coverage: 7x in Q20 bases; sum-of-contigs

estimation

Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.

http://www.hgsc.bcm.tmc.edu/

Center project Information Center project name: GMFA Center clone name: CH230-61K4 Contact: hgsc-help@bcm.tmc.edu

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number be preserved.
GAAAATCAAATTAGAA
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                                                                                                                                                                                                                                                                       даатттаттаалалаататтаалалалалалалалаттаалалалалалалалалалала 215336
                                                                                                                                                                                                                                                                                                                                                                                                                                ATACAAATATTTAAAAATATTATTAAA---AAAACATTCTAAAGTCATTCAGATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u> АДТЪДТАДЬЙТА́ДЬДЬДТАЙАТТАДТАДАЙАЙТТАДДАДАЙАТАТТТАДАДАДАТАТТТАД</u> 21521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTETTGTAAAAACTEAGAGTETTTCAAAACATTCTAATACATGATTAGAGTETATAGAA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCATTAAATATAACACACAAAAAATACATCTAATTATAACAATATATGTTATACATAT 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACACGAGAAACACAATAAACCCACTACCGTCAGGTTATCATAAGGATGAAATGTTTTGAT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACATCTTATTAGAAACTTTTAGTTAAGTCTTGAAGTTAGAATTAAACAAAAAAATTAC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTAGGTTTTCTAGTCATGAGCACCACTCAGAGACAAGATTTCAAGAAAACAATTTTGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is not known and their order in this sequence record is
                                                                                                                   CTCACACCTGTGTGATCATTTAGTCATGTATGTAGTACAATCATTGTAGTTCACAACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241060
241160
242346
242346
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243702
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/mol type="genomic DNA"
/db xref="taxon:10116"
/clone="CH230-61K4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .246611
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47.3%; Pred. No. 2.9e-06;
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Barran, M., Bastien, V., Bloom, T., Boguslavkiy, i., Boukhgalter, B., RS Birren, B., Nusbaum, C., Lander, B., Chaykiy, I., Boukhgalter, B., Barran, M., Bastien, V., Bloom, T., Boguslavkiy, i., Boukhgalter, B., Camar, A., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., Pitzderald, M., Gage, D., Galagan, J., Gardon, S., Ferreira, P., Fitzderald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, I., Grand-Pierre, M., Hafez, N., Hagos, B., Horton, I., Hulme, M., Iliev, I., Johnson, R., Jones, C., Hagos, B., Horton, I., Hulme, M., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Micola, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Minenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Peterson, K., Phunkhang, P., Major, A., Schauer, S., Schupback, R., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Stojanovic, N., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Whan, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
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AC138073
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Birren,B., Nusbaum,C. and Lander,E.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Contact: sequence submissions@genome.wi.mit.edu

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Center project name: L28756

Center clone name: 430_B_7
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="17"
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## ALIGNMENTS

ACCESSION	,	DEFINITION	Focus	CNSOOEVL	RESULT 1
AL069706	BACK29823 of kPC1-98 library from prosopulta metamognosco ( fly), genomic survey sequence.	Drosophila melanogaster genome survey sequence I/ end of Each	CNSOCEVI. 1101 bp DNA linear GSS 04-008-12999		

REFERENCE AUTHORS TITLE JOURNAL Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AL069706.1 GI:4949849

COMMENT

Genoscope.

Direct Submission

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 BVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs, For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of

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FEATURES
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                                         AGGGAAA 672
                                                                              WTATAWITWTATWTATATAWWIAWIAWATATATTTATTAAWWTATATTTTAWAAAWTAA
                                                                                                                                                                                                   CCTCTCACACCTGTGTGATCATTTAGTCATGTATGTAGTACAATCATTGTAGTTCACAAC 605
                                                                                                                                                                                                                                            <u>AANAAAAAAAAAAAAAAWWWWTWATATTWTTATTAAWTWTATWWATTWATTWANT</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster"
|mol_type="genomic_DNA"
|db_xref="taxon:7227"
|cb_ref="BACR29B23"
|clone="BACR29B23"
|clone lib="RPCI-98"
|clone lib="RPCI-98"
|note="end : T7"
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CG749728
CG749728.1 GI:37970654
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Max-Planck-Institute for Deve
Spemannstr. 37-39, Tuebingen
Tel: 00497071601371
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Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode
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Neodiplogasteridae; Pristionchus.
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                                              TCATTAAATATAACACACAAAAAATACATCTAATTATAACAATATATGTTATACATATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="California"
/db xref="taxon:54126"
/db cref="taxon:54126"
/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a part of the genomic DNA with EcoRI and cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Pristionchus
/mol_type="genomic DNA"
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Pred. No. 1.3e-08;
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AL536104.2
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1 (bases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization

Unpublished (2001)
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AL536104 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CSODP022YC18 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Feb 13, 2001 this sequence version replaced Contact: Genoscope Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com l
http://fulllength.invitrogen.com/ InVitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Faraday Avenue Genoscope sequence ID : CS0DF022BB09QP1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACCTGTGTGATCATTTAGTCATGTATGTAGTACAATCATTGTAGTTCACAACAGAGTAA 612
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                                                                                                                                      TTAAGGAAGGTAAGGAAGAAAAAAGATTAAAAAAATGTCCTTATCTCTTTGTTTCTGTA 148
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                         /note=Torgan: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                 /tissue_type="FETAL BRAIN"
/dev_stage="fetal"
                                                                                                                                                                                                                                                                                                                                                               /mol type="mRNA"
/db xref="taxon:9606"
/clone="CSODF022YC18"
                                                                                                                                                                                                                                                                                                                    /clone_
                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
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                                                                                                                                                                               9.0%;
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7
                                                                                                                                                                 Score 103.2; DB 9;
Pred. No. 2.3e-08;
5; Mismatches 171;
                                                                                                                                                                                               DB 9;
                                                                                                                                                                                                 Length 1201;
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On Feb 16, 2001 this sequence version replaced Contact: Genoscope
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1 (bases i to 1201)
Liw.B., Gruber,C., Jessee,J. and Polayes,D.
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9232.f For
more information about this cluster, see
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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Location/Qualifiers
1. 1200
                                                                                                                                                                                                                                                                           /tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Torgan: brain; Vector: pCMVSPORT_6; Ist strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sizes of the pCMVSPORT 6
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/db_xref="taxon:9606"
/clone="CSODF005Y018"
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                                                      8.9%;
              115;
              Score 101.8; DB 9
Pred. No. 4.1e-08;
5; Mismatches 287
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Pristionchus pacificus
Eviatyota, Metazoa; Nematoda; Chromadorea; Diplogasterida;
Budaryota, Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases i to 1391)
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
                                                                                                                                                                                                                                                                       genomic survey sequence
CG754863
CG754863.1 GI:37980782
                                             Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental
Spemannstr. 37-39, Tuebingen D-72076, (
Tel: 00497071601371
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P050-2-G05.za Ppa EcoRI
           Email: ralf.sommer@tuebingen.mpg.
Class: BAC ends.
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                                                                                                                                                                                         Conservative
   sapiens
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/mol type="genomic DNA"

/strain="california"

/db_xref="taxon:54126"

/clone_lib="ppa_BcoRl BAC Library"

/clone_lib="ppa_BcoRl BAC Library"

/note="The library was generated by a partial digest
the genomic DNA with EcoRl and cloning into the BAC
                             GI:30765550
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48.7%;
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Pred. No. 9.3e-08;
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                                          569 TTTTTAAAATATTTAAAAAAAAATWATTAAETTWAATTAAAAAATWTWAAWWWTATWWAA
                                                                                                                                        477
                                                                                                                                                                                                                                                                                686 CTAATTAAAAAMATATWAWTTWWTYWAWTTAATATTTATATTWATTTATAAAAWAWAT 627
                                                                                                                                                                                                                                                                                                                        417 ATATGTTATACATATATTTTGTAAAAACTTAGAGTTTTCAAAACATTCTAATACATGA 476
                                                                                                                                                                                                                                                                                                                                                                          746 TATTAATAWI
                                                                                                                                                                                                                                                                                                                                                                                                                   357 ATGAAATGTTTTGATATCATTAAATATAACACACACAAAAATACATCTAATTATAACAAT 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 TATAATAATTGTAATTAGGTTT-TCTAGTCATGAGCACCACTCAGAGACAAGATTTCAAG 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1200)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAP008BE02CP1.
Location/Qualifiers
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BP 191 91006 EVRY cedex - France
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/tissue type="THYMUS"
/clone I ib="Homo sapiens THYMUS"
/clone I ib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and Cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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/mol_type="mRNA"
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39.5%;
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                                                  307 ATTACACAGAGAAACACAATAAACCCACTACCGTCAGGTTATCATAAGGATGAAATGTT 366
                                                                                                                                                  248 -GITAAACATCTTATTAGAAACTTTTAGTTAAGTCTTGAAGTTAGAATTAAACAAAAAA 306
                                                                                                                                                                                                             667 WIWİKITITÜMAWAAİAAWITITITTATTATTAJAATTTWİAWAAAAWAAATTATTAAAATW 726
                                                                                                                                                                                                                                                             194 AGGTTTTCTAGTCATGAGCACCACTCAGAGACAAGATTTCAAGAAAAACAATTTT-----
                                                                                                                                                                                                                                                                                                                                                                   134 CTCTTTGTTTCTGTAATAATAATAAGAGACTTAAACTTTTAATAATAATAATTGTAATT 193
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1 (bases 1 to 1201)

Li,W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization
Unpublished (2001)
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BP 191 91006 EVRY cedex - France
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                                                                                                        AAWTAAAAATTWTAHAATAAAAATWTAAWTAAATATAAATKTAWATTTWAAAATTTAAT 786
                                                                                                                                                                                                                                                                                                                CCCTKMMHTGYTAAKATAATTATWTKRGTRTTTAAATATAWTMTTWAATWTGTTTGWTAT
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/clone_Tib="Homo sapiens PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/note="Vector; pcMySpORT 6; lst strand cDNA was primed
/note="Vector; pcMySpORT 6; lst strand cDNA was primed."
double-strand cDNA was digested with Not I and cloned i
the Not I and EcRV sites of the pcMySpORT 6 vector.
Library was not normalized."
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Homo sapiens PLACENTA Homo sapiens CDNA clone CSODE014YF05
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/db_xref="taxon:9606"
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    146
                              13
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                                                                                                                                                                                                                                                                                  Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (B-mail: seqref@genoscope.cns.fr) - Web: www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - thtp://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a WRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Prerygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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AL104915.1
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BACN12N03 of DrosBAC library from Drosophila melanogaster (fruit
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Direct Submission
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  GCGAAAATCAAATTAGAAT 685
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larity 45.9%;
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                                                                                                                                                  /clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
                                                                                                                                                                                          /organism="Drosophila melanogaster"
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/mol_type="genomic ZNA"
/db_xref="texxon:7227"
/clone="BACN12N03"
                                                                                                                                                                                                                                                           Location/Qualifiers
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Pred. No. 2.9e-07;
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          /clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial
the genomic DNA with EcoRI and cloning into th
                                                                            /organism="Pristionchus
/mol_type="genomic DNA"
                                                    'db_xref="taxon:54126"
                                                              'strain="California'
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CG745316
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Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterid Meodiplogasteridae; Pristionchus. 1 (bases 1 to 1193) Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Buntjer,J., van der Meulen,M. and Sommer,R.J. genomic survey sequence CG745316 CG745316.1 GI:37966242 GSS Evolutionary Biology
Max-Planck-Institute for Developmental
Spemannstr. 37-39, Tuebingen D-72076, G
Tel: 00497071601371 An integrated physical and genetic map of the Pristionchus pacificus Pristionchus pacificus 00497071601498 BAC ends ralf.sommer@tuebingen.mpg Sommer RJ Location/Qualifiers Genomics 269 (5), Chromadorea; Diplogasterida; 715-722 pacificus" Germany (2003)nematode Pristionchus Jansen, K.,

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BX462207 Homo sapiens B CELLS (RAMOS CELL LINE) Homo
clone CSODG004YB03 5-PRIME, mRNA sequence.
BX462207
       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                                               EST
                                                              Homo sapiens
                                                                                        BX462207.1 GI:31023422
Contact: Genoscope
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BP 191 91006 EVRY cedex - France
Email; segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 24.r For modernation about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODG004CA02QP1&cluster=24.r. Contact:
Peng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODG004CA02QP1.
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                                                                                                                                                                                                                                                                                                                                                                           <u> АДДВААДДААДААДААДААДАДААДАДАТЗАҮДАЖАДАДАДАДАДАДАДАДТТТТТАДА</u>
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Conservative
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/cell_line="RAMOS_CELL_LINE"
/clone_lib="Homo sapiens B_CELLS (RAMOS_CELL_LINE)"
/clone_lib="Homo sapiens B_CELLS (RAMOS_CELL_LINE)"
/note="Wector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and scored i
the Not I and BCORV_sites of the pCMVSPORT 6 vector.
Library was not normalized."
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/db_xref="taxon:9606"
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0; Mismatches 287
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com t
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAPOOBCA01QP1.
Location/Qualifiers
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5-PRIME, mRNA sequence.
BX437758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                    TCATAAGGATGAAATGTTTTGATATCATTAAATATAACACACAAAAAATACATCTAATT
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/db_xref="taxon:9606"
/dlone="CSOCAP008YB01"
/clone="CSOCAP008YB01"
/clone=lb="Homo sapiens THYMUS"
/clone="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned ithe Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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18; Pred. No. 3e-07;
120; Mismatches 291;
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Best Local
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 293
                                    468
                                                                                                                                                                              348 ААТТСААААААСАААААЖТАТААААМАААААААКТААААААААТWTAAATTAAAA
                                                                                                                                                                                                                                                   53 AACAGTTAACAAACAAATTTATGTTTCATTTGAGATTAAGGAACGTAAGGAAGAAAAAA 112
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BX436885
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Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.co
http://fulllength.invitrogen.com/ InvitroGen Corporation 16
Faraday Avenue Genoscope sequence ID: CSOCAP004AB05QP1.
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Contact: Genoscope
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Mammalia; Eutheria;
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BP 191 91006 EVRY cedex - France
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ATTAAACAAAAAAATTACACACGAGAAACACAATAAACCCACTACCGTCAGGTTATCAT 352
                                AAAAAATAAAWTTYATAYWAAAAAAAAAAAATAAWAAAATTTAAATTTTTATAAAWA
                                                                                                       ТТЖАЛТАЛАЛАЛАЛАТЛАЛАЛАЛТЖТАМАЛАНАЛАЛАТТАЛАЛАЛАЛАЛАЛАЛАТА 467
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                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/mol type="mRNA"
/mol type="mRNA"
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/clone lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Homo sapiens THYMUS
mRNA sequence.
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BH183498
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Le Paslier,M.C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W., Williams,D.L., Johnston,D., LoVerde,P.T. and Le Paslier,D. Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library

Genomics 65 (2), 87-94 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schistosoma mansoni
                                                                                                                                                                                                                                            Institut Pasteur de Lille
1 rue du Professeur A. Calmette, 59019-
1 rue du Professeur A. Calmette, 59019-
Tel: (33) (0)3 2087788

Tex: (33) (0)3 20877888

Email: Raymond.Pierce@pasteur-lille.fr
CNS sequencing ID-BGOAM023CF04BP1

Plate: 023 row: L column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma
1 (bases 1 to 660)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BH183498.1
                                                                                                                                                                                                                Seq primer: M13 reverse primer Class: BAC ends
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Contact: Pierce RJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u> АДБАЙ</u>САМАДАЛАТТТУАЛЛАЛАЛАЛАЙАЙАЛАЛАЛАЛАЛАЛАЙАЙАЙТАКТТАЛА
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/clone_lib="SmBAC1"
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/strain="puerto-Rican"
/db_xref="taxon:6183"
                                                                                                                                                                               ocation/Qualifiers
                                                                   sex="mixed"
                                                                               clone="023107"
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   pBeloBAC 11; Site_1: Hind III; Partially
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ne 023L07 5',
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<u> АГТТАААААТАТАТТТТАААААААСАТТСТАААСТСАТТСАСАТССТСТСАСАССТСТ</u>
                                                                                                                                                                            <u> АДАҚАДАДАДАЛАЛАЛАЛАДАДАҚ</u>ҚАҚАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА
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44.08;
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Pred. No. 4 9e-07;
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44
Schistosoma mansoni

Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 [bases 1 to 660]

1 [bases 1 to 660]

1 [baseler, M.C., Pierce, R.J., Merlin, F., Hirai, H., Wu, W.,

Williams, D.L., Johnston, D., Loverde, P.T. and Le Paslier, D.

Construction and characterization of a Schistosoma mansoni
                                                                                                                                                                                                  AL620449
AL620449.1 GI:16034591
GSS
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T3 end of clone 023CF04 of library SmBAC1 from strain Puerto-Rican
of Schistosoma mansoni, genomic survey sequence.
                                                                                                                                                                               Schistosoma mansoni
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Partially Hind III digested and size-selected S. mansoni cercarial

DNA was ligated into Hind III digested pBeloBAC II vector and used

to transform E. coli DH10B. The complete library contains 23808

clones from 4 independent sizing-ligation-transformations. Average

insert size ranges from 70-127 kb and genome coverage is 7.9-fold.

Location/Qualifiers
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Genomics 65 (2), 87-94 (2000)
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(mol type="genomic DNA"
/strain="Puerto-Rican"
/db xref="taxon:6183"
/clone="023CE04"
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/note="end : T3"
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Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L.,
Buntjer, J., van der Meulen, M. and Sommer, R. J.
An integrated physical and genetic map of the nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic survey sequence CG749499 CG749499.1 GI:37970425
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Max-Planck Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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Neodiplogasteridae; Pristionchus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Sommer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest
the genomic DNA with EcoRI and cloning into the BAC
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/mol_type="genomic DNA"
/strain="California"
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637 TATATAATATATACAATTAAATAAAAAAGGGAAAATCAAATTAGAA 684 	577 TATGTAGTACAATCATTGTAGTTCACAACAGAGTAAAATAAAT	517 TTAAAAAAAACATTCTAAAGTCATTCAGATCCTCTCACACCTGTGTGATCATTTAGTCATG 576	457 CAAAACATTCTAATACATGATTAGAGTTTATAGAAATACAAATATTTAAAAAATATAATT 516

Search completed: June 2, 2004, 03:32:47 Job time: 3393 secs

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Sequence:
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                   d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
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Gapop 10.0 , Gapext 1.0
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1148
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GenCore version (c) 1993 - 2004
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           US-10-204 708-20
US-08-998-416-288
US-08-998-416-1137
US-10-204-708-32
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US-10-204-708-50
US-10-204-708-50
US-10-204-708-50
US-10-204-708-50
US-10-204-708-50
US-10-204-708-50
US-07-991-867B-32
US-08-544-332-32
US-08-544-332-8
US-08-370-861A-32
US-08-370-861A-32
US-08-370-861A-32
US-08-370-861A-32
US-08-370-861A-32
US-08-370-861A-32
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Compugen Ltd
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Sequence 1137, Ap
Sequence 32, Appli
Sequence 2, Appli
Sequence 13, Appli
Sequence 14, Appli
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Sequence 32, Appli
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Sequence 63, Appl
Sequence 20, Appl
Sequence 28, Appl
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	5.1	5,1	5.1				5.2		5.2	5.2	5. 2	5.2	5.2	5 2	5. 2	5.3	5.3	
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### ALIGNMENTS

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RESULT 1

US-08-487-8258-13

Sequence 13, Application US/08487826B

Patent No. 593887

REPLICANT: Sim, Kim L.

APPLICANT: Willer, Lowis H.

ANDHESSEE: Knobbe Martens Colson & Bear

STREET: 620 Newport Beach

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STREET: 620 Newport Center Drive 16th Floor

COMPUTER READABLE FORM:

MEDIUM TYRE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYRE: Floppy disk

COMPUTER PREADABLE FORM:

MEDIUM TYRE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYRE: Floppy Application #1.25

ZIP: 92660

ZIP: 92660

CURRENT APPLICATION DATA: 10-005/MS-00S

SOFTMARS: PRESIDENT NEORMATION:

NAME: 1stablent Neormation:

MARK: 1stablent Neormation:

MARK: 1stablent Neormation:

MARK: 1stablent Neormation:

MARK: 1stablent Neormation:

TELEPHONE: (619) 235-0376

FREGRENCE/DOCKET NUMBER: 29 655

REGISTRATION INFORMATION:

SEQUENCE CHARACTERISTICS:

ENDING: No. 13:

SEQUENCE CHARACTERISTICS:

LEWTH: 1924 base pairs

TYPE: Nucleic acid

STRANDBURSS: single

STREET No. 2018

MUSCON 2019

MUSCON 2019

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Query Match Best Local Similarity

48.3%;

Score 74; DB 2; 1 Pred. No. 2.8e-07;

Length 19124;

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RESULT 2
US-08-232-463-14
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                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC-compatible
OPBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                       STATE: V
                                                                                                                                                                                                                                           STREET: 1800 Dia:
CITY: Alexandria
    APPLICATION NUMBER: US/08/232,463 FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16084 ATATATATATATATATATATATATATATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15667 АЛАЛАНСАТТЕЛЬНЬАЛЬЛЬЛЬЛЬЛЬНАТАТАТАТАЛЬЛЬНСЕЛЬНЬАЛЬЛЬНЬАЛЬНЬАЛЬНЬАЛЬНЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      521 AAAAACATTCTAAAGTCATTCAGATCCTCTCACACCTGTGTGATCATTTAGTCATGTAIG 580
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5670367
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1800 Diagonal Road, Suite 500
                                                                                                                                                                                                         USA
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US-10-204-708-63/c
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                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
                                                                                                                                                                                                                                                                                                                                           Sequence 63, Application US/10204708
Patent No. 6677731
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: line
IMMEDIATE SOURCE:
CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1427 YYYYYYGTACCAAATTCTTCTATCTTTAACTACTTGCATAGATAG 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                985 AATTTAAACTAATTATTTCATATACTTTTTTGATGACGTGGATGCATTG 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    925 CACTCCTCTCACTTCCCATTGCTACCTGCCAAACCGCTTCTCTCCATAAATATCTATTTA 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     745 CCACACATGTCTCACTTTCGACTTTGGCTTTTTCACTATGACACAACTCGCCATG 804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACCTCAGCTCCCACCTCTTCTCATTATGAGCCTACTGGCCATGCACACCTGCCACCTCAG 924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (703)836-9300
(703)683-4109
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APPLICANT: OLEK, Alexander
APPLICANT: DIESENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated wit
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: PCTIEPO1/03971
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
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US-10-204-708-20/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 63
LENGTH: 5562
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/10204708 Patent No. 6677731
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Best Local Similarity 47.4%;
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PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
ij
  NO 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             АВАСАСТАТААААААСААААААТААТААААААААААТСТААСТААСАААААТААА
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Pred. No. 5.2e-07;
0; Mismatches 240
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; OTHER INFORMATION: US-10-204-708-20
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Best Local S
Matches 205
                                                                                                                                                                                                 Sequence 288, Applica Patent No. 6239264 GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                            APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENCMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USBS THERBOF
                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                        APPLICANT:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
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                                                                                                                                                                                                                                                                                                                                                                            ДАДАДАДАДАДАССЬВАВАНТАЛАДСЬТТСАССАВАДСТВТАТТВАДАДАДССЬТВАВАТС
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATATCGAAAAAAATCTAAATAAAAATAACGAAAAATCCTAAAATTAACCATTAAAA
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                                                                                                                                           Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
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                                                                                                                    Wendland, Jurgen
Knechtle, Philipp
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48.0%;
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Pred. No. 6.2e-07;
0; Mismatches 222;
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ZIE: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MG-DOS
OPERATING SYSTEM: PC-DOS/MG-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:

APPLICATION NUMBER:

US/08/998,416

COUNTRY: US ZIP: 27709

USA

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639
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                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 339;
                                                                                                                   PP/5-30306/A/CGC1976
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FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION WUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                    NAME: Meigs, J. Timochy
REGISTRATION NUMBER: 38,241
RELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
INFORMATION FOR SEQ 10 NO: 288:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1241RP
                                                                                                                                                                                                                                                                                                                                            6.1%;
                                                                                                                                                                                                          LENGTH: 837 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                         Matches 285; Conservative
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                                                                                                                                                                                                                                                                                                                                                          Similarity
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Best Local S
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RESULT

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Sequence 6, Application US/10204708

Sequence 6, Application US/10204708

Patent No. 6677731

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: DIEPERBROCK, Christian
APPLICANT: DIEPERBROCK, Christian
APPLICANT: DIEPERBROCK, Christian
APPLICANT: DIEPERBROCK, Christian
APPLICANT: BERLIN, Kurt
ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT APPLICATION NUMBER: US 10019058.8
PRIOR FILING DATE: 2001-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 100195259.7
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6135 ACTTCATAAAAAAAAAAAACTAAAAAAACCACTACTAAACTTAAAAATTATATATATT 6076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6075 TABABATACABATACTABABATAATTABABATCCCABABAACTAACAAA---AA 6019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCACAAATAACAAAAATTTTTTATTTATAAATTACAATTTACTTAAAAATAAAA 6194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAATATATATACATATATTTTTTTTTAAAAACTTAGAGTTTTTCAAAACATTCTAATA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITTAATATAATAATTGTAATTAGGTTTTCTAGTCATGAGCACCACTCAGAGACAAGATT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAAGAAAACAATTTTGTTAAACATCTTATTAGAAACTTTTAGTTAAGTCTTGAAGTTAG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 AATTAAACAAAAAATTACACACGAGAAACACAATAAACCCACTACCGTCAGGTTATCA 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 6669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.7%; Pred. No. 3.9e-06;
Matches 241; Conservative 0; Mismatches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
US-08-998-416-1137/c
, Sequence 1137, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6018
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us-10-015-637-1.rni

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Sequence 32, Application US/10204708

Factor No. 6677731

GENERAL INPORMATION:
FACTORY: Alexander
APPLICANT: OLER, Alexander
APPLICANT: OLER, Alexander
APPLICANT: DISPENBRCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Dy Assessing DRA Methylation
FILE REFERENCE: 5013.1012
CURRENT FILING DATE: 2003.65-66
FRIOR APPLICATION NUMBER: PCT/EP01/03971
FRIOR APPLICATION NUMBER: PCT/EP01/03971
FRIOR PILING DATE: 2000-04-06
FRIOR FILING DATE: 2000-04-07
FRIOR FILING DATE: 2000-04-07
FRIOR FILING DATE: 2000-04-07
FRIOR FILING DATE: 2000-06-30
FRIOR FILING DATE: 2000-06-30
FRIOR FILING DATE: 2000-08-01
FRIOR FILING DATE: 2000-08-01
FRIOR FILING DATE: 2000-08-01
FRIOR FILING DATE: 2000-08-01
FRIOR FILING DATE: 2000-08-01
FRIOR FILING DATE: 2000-08-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           437 TOTAAAAACTTAGAGTTTTTGAAAAGATTCTAATACATGATTAGAGTTTATAGAAATACA 496
336 ATTTTAATAAACAATTAATAATAATATATTAATTATTGATAATCTATTTAATAATTTAT 277
                                                     490 AAATACAAATATTTAAAAATATATATATTTTAAAAAACATTCTAAAGTCATTCAGATCCTC 549
                                                                                                  276 TAAAGAAAATAATATTATTAATAATATTTTAATAACTAATTTAAAATTTGAACATAGAC 217
                                                                                                                                                  550 TCACACCTGTGTGATCATTTAGTCATGTATGTACAATCATTGTAGTTCACAACAGAG 609
                                                                                                                                                                                                  197 TTTTCTAGTCATGAGCACCACTCAGAGACAAGATTTCAAGAAAACAATTTTGTTAAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317 AGAAACACAATAAACCCCACTACCGTTATCATAAGGATGAAATGTTTTGATATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2237 CAAAATACACCTAAACGTTATATCAATTATTTTTATTAAAATCAATTAATAACGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 TAAATATAACACACACAAAAATACATCTAATTATAACAATATATATGTTATACATATATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 CTTATTAGAAACTTTTAGTTAAGTCTTGAAGTTAGAATTAAACAAAAAATTACACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 8093;
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                                                                                                                                                                                                                                                                                                                                                            670 AAAATCAAATTAGAATTTTTGAT 692
                                                                                                                                                                                                                                                                                                                                                                                                          96 ATAATGATAATAATAGTTTAAAT 74
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 46.2<sup>3</sup>
Matches 222; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATTAGGTTTTCTAGTCATGAGCACCACTCAGAGACAAGATTTCAAGAAAACAATTTTGT
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                                                                                                                                                                               SEQUENCES OF ASHBYA GOSSYPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.8%; Score 67; DB 3; Length 636; Best Local Similarity 44.9%; Pred. No. 3.5e-06; Matches 253; Conservative 0; Mismatches 310; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION DATA:
PULLING DATE: 24-DEC-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: MAME: PROGRATION: PF/5-30306/A/CGC1976
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 1137:
SEQUENCE CHARACTERICE:
SEQUENCE CHARACTERICE:
TELEPHONE: 676 has paire
                                                                                                                                                                                                                                                                                     3: No. 6239264artis Corporation 3054 Cornwallis Road
                                                                             APPLICANT: MODE, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUEN
TITLE OF INVENTION: AND USES THEREOF
UNDRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporat
                                                                                                                                                                                                                                                                                                                                  CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                             Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1692RP
             Philippsen, Peter
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
1585 CCTATTTTATAAATAAAACTTCATAATAAATAAATTATAAATAAAATTTTACATATAT 1526
                                                                                                                                       1405 ataataaaattaaaaaaaaaactaaacaaaccaattatataaca---aaaaataaaata 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               631 AGGGAATATATATATATATACAATTAAATAAAAAAGGGAAAATCAAATTAGAATTTTTG 690
                                                                   391 ACAAAAATACATCTAATTATAACAATATATGTTATACATATATTTTTTGTAAAAACTTAGA 450
                                                                                                                                                                                                           451 GTTTTTCAAAACAFTCTAATACATGAFTAGAGTTTAFTAGAAATACAAATATTTAAAAAAT 510
                                                                                                                                                                                                                                                                                                                                                       511 ATAATTTTAAAAAACATTCTAAAGTCATTCAGATCCTCTCACACCTGTGTGATCATTTA 570
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
CLASSIFICATION: 435
TYONNOW ASTERMENT TO A TO THE TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A TOWN ASTERMENT A T
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620 Newport Center Drive 16th Floor
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GENERAL INFORMATION;
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ATTORNEY/AGENT INFORMATION:
NAME: 1sraelsen, Ned
REGISTRATION NUMBER: 29,655
REPRENCE/DOCKET NUMBER: NIH1).
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-655
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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Chitnis, Chetan
Miller, Louis H.
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TYPE: nucleic acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Mai
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: California
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MOLECULE TYPE: (
HYPOTHETICAL: NC
ANTI-SENSE: NO
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Xurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dy Assessing DNA Methylation
TITLE OF INVENTION: LOS 1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/FP01/03971
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR PRILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-06-07
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-2
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5.7%; Score 65.8; DB 4; Length 10;
Best Local Similarity 45.2%; Pred. No. 1.6e-05;
Matches 284; Conservative 0; Mismatches 342; Indels
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Patent No. 6677731
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Patent No. 6677731
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: DIEFENBROCK, Christian
APPLICANT: BREIN, Kurt
APPLICANT: BREIN, Kurt
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                                                                                                                                                                                                                                                                       Score 64.8; DB 4; Length 6 Pred. No. 2.2e-05; 0; Mismatches 362; Indels
                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA
108-10-204-708-50
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                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 46.3%;
Matches 315; Conservative
2000-09-01
S: 98
PRIOR FILING DATE: 200
NUMBER OF SEQ ID NOS:
SEQ ID NO 50
LENGTH: 6306
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US-10-204-708-12/c
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                                                                                                                                                                                                                   aattaaaaggaataagttaaataaaattaagaaattagttatattttatäaaaataaca 18220
                                                                                                                                                                                                                                                                                                                                                                                                                                      18159 ATAAATAATTTTTATATGAGATTATATATTTTTTTTGGCTGGATTATTCAGAATTAGA 18100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18099 GTÄÄCAAAATTÄÄÄACACATÄTATAÄÄÄCACATÄTATÄÄÄTACACATTTAAÄTÄTÄÄT 18040
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                                                                                                                                                               60 AACAAAACAAATTTATGTTTCATTTGAGATTAAGGAAGGTAAGGAAGAAAAAAGATTAAA 119
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                                                                                                                                                                                                                                                                             AAAAATGTCCTTATCTCTTTCTGTAATAATAATAAAAGAGACTTAAACA
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                                                    Length 19124;
                                                    Score 65.8; DB 2; Length 1
Pred. No. 1.9e-05;
0; Mismatches 357; Indels
                                                       5.78;
                                                                                 Best Local Similarity 44.8
Matches 291, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-10-204-708-50/c
  US-08-487-826B-13
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FILE REFERENCE: 5013.1012

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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 AATGTTTTGATATCATTAAATATAACACACAAAAATACATTATTAAAATATAT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 GTTATACATATATTTTGTAAAACTTAGAGTTTTTCAAAACATTCTAATACATGATTAG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S ATCCTTCAATAGAAATGTGTTATTTCCTCATCACCAGACAAGGGGCAACAGTTAACAA
                                                                                                                                                                                                                                                                                                                                                                                                              185 ATTGTAATTAGGTTTT----CTAGTCATGAGCACCACTCAGAGAGATTCAAGAAAA
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                                                                                                                                                                                                                                                        ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                Query Match 5.6%; Score 64.6; DB 4; Length 6317; Best Local Similarity 46.4%; Pred. No. 2.5e-05; Matches 319; Conservative 0; Mismatches 359; Indels 9
FILE KEREAGALE: 3013.1012
CURRENT PAPELICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PETERD1/03971
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 12
LENGTH: 6317
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                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                             FEATURE:
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APPLICANT: OLEX, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BELLIM, Gutt
ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
FILE REPERENCE: 5013-1012
CURRENT APPLICATION NUMBER: US/10/204, 708
CURRENT APPLICATION NUMBER: US/10/3971
RIOR APPLICATION NUMBER: DE 10019058.8
RIOR APPLICATION NUMBER: DE 10019058.8
RIOR APPLICATION NUMBER: DE 10019173.8
RIOR APPLICATION NUMBER: DE 10019173.8
RRIOR APPLICATION NUMBER: DE 10019173.8
RRIOR APPLICATION NUMBER: DE 10032529.7
RRIOR APPLICATION NUMBER: DE 10043826.1
RRIOR PILING DATE: 2000-06-30
RRIOR APPLICATION NUMBER: DE 10043826.1
RRIOR PILING DATE: 2000-06-30
RRIOR APPLICATION NUMBER: DE 10043826.1
RRIOR PILING DATE: 2000-09-01
RRIOR PILING DATE: 2000-09-01
RRIOR PILING DATE: 2000-09-01
RRIOR SEQ ID NOS: 98
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US-10-204-708-54
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JS-10-204-708-54/c
; Sequence 54, Application US/10204708
; Patent No. 6677731
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ORGANISM: Artificial Sequence
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US-08-107-755A-32/c
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                                                                                                                  APPLICANT: MOYET, Richard W.
APPLICANT: MOYET, Richard L.
APPLICANT: Hall, Richard L.
APPLICANT: Hall, Richard L.
APPLICANT: Hall, Richard L.
APPLICANT: Graid, Michael E.
APPLICANT: Graid, Michael E.
APPLICANT: SEQUENCES: 66
CORRESSPONDEWCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 63.8; DB 1; Length 66 Pred. No. 1.8e-05; 0; Mismatches 277; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION NUMBER: W 09/4818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W 07/827,685
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAILWANDINK, DAVIG R.
REGISTRATION NUMBER: UP114.C3
TELEDENOMULICATION INFORMATION:
NAME: 941-375-5100
TELEDENOMULICATION INFORMATION:
TELEDENOMULICATION INFORMATION:
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TELEDENOMULICATION INFORMATION:
TELEDENOMULICATION INFORMATION:
TELEDENOMULICATION INFORMATION:
                                              Sequence 32, Application US/07991867B
Patent No. 5476781
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 48.5%;
Matches 272; Conservative (
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TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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nucleic acid
EDNESS: double
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COUNTRY: USA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,755A
FILING DATE: 19-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/827,658
FILING DATE: 30-JAN-1992
PRIOR APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORIEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 31,794
REPERENCE/DOCKET NUMBER: UF114.C2
TELECONGUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 48.5%; Pred. No. 1.8e-05;
Matches 272; Conservative 0; Mismatches 277; Indels 12; Gaps
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Search completed: June 2, 2004, 02:26:17 Job time: 112 secs

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2, 2004, 01:00:19 ; Search time 538 Seconds (without alignments) 9064.928 Million cell updates/Bec
GenCore version 5.1.6
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US-10-015-637-1 1148 1 taggatccttcaatagaaaa......agagagtgatggttaatgca 1148 3373863 segs, 2124099041 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 score: Scoring table: Sequence: Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

6747726

Post-processing: Minimum Match 0%
Maximum Match 160%
Listing first 45 summaries

genesegn2003bs:\* genesegn2003cs:\* geneseqn2003as:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn2004s:\* N\_Geneseq\_29Jan04:\* 1: geneseqn1980s:\* genesegn1980s:\* genesegn1990s:\* geneseqn2000s:\* geneseqn2002s:\* 10: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description		Abn83929 Arcelin-5	Aad29066 Phaseolus	Abn83917 Truncated	Abn83928 Arcelin-4	Abn83927 Arcelin-3	Abz10246 Haematopo	Abz10199 Haematopo	Abk87142 Scarlet r	Abn83926 Arcelin-5	Abz10100 Haematopo		Aaq94051 Kidney be	Abl33576 Human imm	Aas46748 Tumour su	Abz10188 Haematopo	Ade84162 Human lym	Abl34157 Human imm	Abz10053 Haematopo	Abk39932 Human che	Abl70139 Chemicall	Abl33958 Human imm	Abg67002 Human ang
αı	ABN83916	ABN83929	AAD29066	ABN83917	ABN83928	ABN83927	ABZ10246	ABZ10199	ABK87142	ABN83926	AB210100	ABZ10246	AAQ94051	ABL33576	AAS46748	ABZ10188	ADE84162	ABL34157	ABZ10053	ABK39932	ABL70139	ABL33958	ABQ67002
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& Query Match	100.0	100.0	99.7	97.7	69.4	69.3	۲. 9.	7.6	7.4	7.4	7.4	7.4	7.4	7.3	7.2	7.2	7.2	7.2	7.1	7.1	7.1	7.0	7.0
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ABQ67093	ABZ10100	AAS46815	AAX33181	ABL33697	AAX33182	AAX33180	ABK40056	AAX33184	AAS46704	AAS46429	ABK40031	ABL33472	ABQ15588	ABQ15589	ABL34358	ABL32808	AAS46623	ABL33874	ABL33307	ABL34155	ABL33949	
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## ALIGNMENTS

Truncated P. vulgaris exotic genotype G02771 Arcelin-5 promoter sequence. ABN83916 standard; DNA; 1148 BP (first entry) 06-SEP-2002 ABN83916; RESULT 1 ABN83916 

Arcelin-5; promoter; plant; transgenic; soybean; agriculture; nutrition; pharmaceutical; ds.

Phaseolus vulgaris. W0200250295-A2.

27-JUN-2002.

17-DEC-2001; 2001WO-US047495. 18-DEC-2000; 2000US-0255879P. (RENE-) RENESSEN LLC.

New transformed or transgenic soybeans plants or cells with an Arcelin-5 promoter, for use as an improved diseary source of protein for humans or animals, or for producing soybeans with important agricultural or nutritional properties. WPI; 2002-508809/54.

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Oulmassov

Dubois P, Liang J,

Wang Q,

Claim 4; Page 65-66; 74pp; English.

The invention relates to a transformed soybean plant cell and transgenic soybean plant, both of which has a nucleic acid molecule comprising the phaseolus vulgaris exotic genotype 02071 Arcelin-5 promoter sequence. The transformed soybean plant cell and transgenic soybean plant are useful as an improved source of dietary protein for humans and livestock. These are also useful for producing soybean plants that exhibit important agricultural, nutritional or pharmaceutical properties. The current sequence represents the truncated P. vulgaris exotic genotype 002771 Arcelin-5 promoter sequence. This sequence is a deletion mutant of the Arcelin-5 promoter, created by the removal of approximately 600 base

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humans or
or
                                                                                                                                                                                                                                                                                                                                                                Arcelin-5; promoter; plant; transgenic; soybean; agriculture; nutrition; pharmaceutical; ds.
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                                         CGNGGATGCATTGCCATCGTTTAATAATTGTTAATTTGGAGTTGAATAATAAATGA
                                                           Gaps
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100.0%; Pred. No. 4.6e-190;
ive 0; Mismatches 0; Indels 0;
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Matches 1148; Conservative
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                                                          Length 1148;
                             Sequence 1148 BP; 420 A; 211 C; 155 G; 362 T; 0 U; 0 Other;
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llarity 100.0%;
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The invention relates to heterologous gene expression in plants. The invention also relates to seed preferred expression cassette having gene regulatory elements comprising arcelin promoter, arcelin 51 leader, and arcelin 51 s' end. This expression cassette is useful for heterologous gene expression in plants. The protein encoded by the heterologous gene expression in plants. The protein encoded by the heterologous gene is a single chain antibody variable fragment (scrv). The present sequence is phaseolus vulgaris arcelin promoter of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                         Novel seed preferred expression cassette having gene regulatory elements comprising arcelin promoter, arcelin 51 leader, and arcelin 51 3' end, useful for heterologous gene expression in plants.
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                                                                                                                                             Heterologous gene expression; plant; arcelin promoter; arcelin leader; seed preferred expression cassette; ds.
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                                                                                                                   Phaseolus vulgaris arcelin promoter
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Matches 1146; Conservative
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Arcelin-5 humans or or

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The invention relates to a transformed soybean plant cell and transgenic soybean plant, both of which has a nucleic acid molecule comprising the blaseolus vulgaris exotic genotype 60271 Arcalin-5 promoter sequence. The transformed soybean plant cell and transgenic soybean plant are useful as an improved source of dietary protein for humans and livestock. These are also useful for producing soybean plants that exhibit important sequence represents a truncated P. vulgaris exotic genotype 602771 Arcelin-5 promoter sequence. This sequence was used in the expression of a GUS reporter gene in a soybean cotyledon
                                                                                                                      New transformed or transgenic scybeans plants or cells with an promoter, for use as an improved dietary source of protein for animals, or for producing scybeans with important agricultural
                                                                                                                                                                 Example 5; Page 66; 74pp; English.
                                       17-DEC-2001; 2001WO-US047495
                                                       18-DEC-2000; 2000US-0255879P
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                      Length 1122;
Sequence 1122 BP; 410 A; 210 C; 146 G; 356 T; 0 U; 0 Other;
                                             0; Indels
                     97.7%; Score 1122; DB 6; I
100.0%; Pred. No. 1.4e-185;
ive 0; Mismatches 0;
                                    Best Local Similarity 100.
Matches 1122, Conservative
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Arcelin-5; promoter; plant; transgenic; soybean; agriculture; nutrition; pharmaceutical; ds.

Phaseolus vulgaris.

Truncated P. vulgaris exotic genotype G02771 Arcelin-5 promoter #2.

(first entry)

06-SEP-2002

us-10-015-637-1.rng

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               Arcelin-4; promoter; plant; transgenic; soybean; agriculture; pharmaceutical; ds.
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                                                               The invention relates to a transformed soybean plant cell and transgenic soybean plant, both of which has a nucleic acid molecule comprising the phaseolus wilgaris exotic genotype 602/71 Arcelin-5 promoter sequence. The transformed soybean plant cell and transgenic soybean plant are useful as an improved source of dietary protein for humans and livestock. These are also useful for producing soybean plants that exhibit important agricultural, nutritional or pharmaceutical properties. The current sequence represents an arcelin-4 full length promoter sequence
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promoter, for use as an improved dietary source of protein for animals, or for producing soybeans with important agricultural
                                                                                                                                                                                            Score 796.6; DB 6; Length 1866;
Pred. No. 3.9e-129;
0; Mismatches 99; Indels 78;
                                                                                                                                                                      Sequence 1366 BP; 692 A; 339 C; 209 G; 626 T; 0 U; 0 Other;
                                              Example 1; Fig 4; 74pp; English
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Best Local Similarity 85.4%;
Matches 1034; Conservative
                         nutritional properties.
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qu	1410	CCTCAGCTCCCTCCTCCACACACTCTCATCTTCGACTTTGGCTTTTCACTA 146	69
ठे	788	TGACACAACTCGCCATGCATGTTGCCACGTGAGCTCCTTCCT	
qq	1470	GEAGACAACTCGCCATGCACGCCACGCCACGTCCTTCCTTTCCCATGATGACACA 152	29
È	848	CTGGGCATGCATGCTGCCACCTCAGCTCCCACTCTTCTCATTATGAGCCTACTGGCCAT 907	7
Db	1530	CFGGGCAFGCATGACCACCTCAGCTCCCACCTCTTCTCATTATGAGCCTACTGGCCAT 1589	89
à	806	GCACACTGCCACCTCACTCTCACTTCCCATTGCTACCTGCCAAACCGCTTCTCT 967	7
DP DP	1590	GCACACTGCCACCTCACTCCTCTCACTTCCCATTGCTACCTGCCAAACCGCTTCTCT 1649	49
à	968	CCATABARAICTAFTTAAATTTAAACTAATTATTTCATATACTTTTTTGAFGACGTGGAT 1027	27
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'n	1138	TGGTTAATGCA 1148	
qq	1830		

ABN83927 standard; DNA; 1872 BP

(first entry) 06-SEP-2002

Arcelin-3 full length promoter sequence.

Arcelin-3; promoter; plant; transgenic; soybean; agriculture; nutrition; pharmaceutical; ds.

Phaseolus vulgaris.

27-JUN-2002.

17-DEC-2001; 2001WO-US047495

18-DEC-2000; 2000US-0255879P

(RENE-) RENESSEN LLC

New transformed or transgenic soybeans plants or cells with an Arcelin-5 promoter, for use as an improved dietary source of protein for humans or animals, or for producing soybeans with important agricultural or Wang Q, Dubois P, Liang J, WPI; 2002-508809/54.

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Oulmassov

Example 1; Fig 4; 74pp; English.

nutritional properties.

The invention relates to a transformed soybean plant cell and transgenic soybean plant, both of which has a nucleic acid molecule comprising the Phaseolus vulgaris exotic genotype 02771 Arcelin-5 promoter sequence. The transformed soybean plant cell and transgenic soybean plant are RESULT 6

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useful as an improved source of dietary protein for humans and livestock. These are also useful for producing soybean plants that exhibit important agricultural, nutritional or pharmaceutical properties. The current sequence represents an arcelin-3 full length promoter sequence និនិនិនិនិនិនិ

Sequence 1872 BP; 694 A; 339 C; 209 G; 630 T; 0 U; 0 Other;

945 ABACATCTTATTAGABACTTTTAGCBAGTCTTTGBAGTTAGBATTBARCBABAAATTTAC 1004 1065 ATACCATTAAATATAACACACACAAAAATACATGTAATTATAAACAATACATGTTATAC-- 1122 1241 1409 1005 ACACACGAAGAACACAATAAACCTATCGTCAGGTTATCATAAGGATGAAATGTTTTG 1064 1123 ATATTTTTGAAAAACTTAAAGTTTTTGAAAACATTCTTAATACATGATTAGAGCTTATA 1182 1349 1469 118 1242 cricacaccegicaaaricarrracregracraracracerercaraaracricacaacae 1301 143 250 429 704 884 944 251 AAACAICTTATTAGAAACTTTTAGTTAAGTCTTGAAGTTAGAATTAAACAAAAAAAT-T 309 369 488 548 607 667 727 787 907 885 TTAGTCAGGAGTGTATCCTCACCCCTCACAAACAATTCAAGAAACAATTTGTT 645 TAGGATCCTTCAATAGAAAATGTGTTATTTCCTCATCACCAGGAAAAAAAGGACAACAGT 119 AAAAAATGICCTTATCTCTTTGTTT -----CTAGTCATGAGCACCACTCAGAGACAAGATTTCAAGAAACAATTTTGTT 1 TAGGATCCTTCAATAGAAAATGTGTTATTTCCTCATCACCAG--ACAAAGGGGCAACAGT 144 -CTGTAATAATAATATAAGAGACTTAAACTTTTAATAATAATTGTAATTAGGTTTT--310 ACACACGAGAAACACAATAAACCCACTACCGTCAGGTTATCATAAGGATGAAATGTTTTG ATATCATTAAATATAACACACACACAAAAATACATCTAATTATAACAATATATGTTATACAT ATATTTTRGTAAAAACTTAGAGGTTTTTCAAAACATTC-TAATACATGATTAGAGTTTATA CTCACACCTGTGTGATCATTTAGTCAT-GTATGTACTACAATCATTGTAGTTCACAGG AGTAAAAAGAATAAGAATAAACTAGTGAATATA-------AAATTITATAAAAG GGAAAATCAAATTAGAATTTTTGATTCCCCACATGACACACTCACCATGCACGCTGCCA 1410 ccrcascroccrocrocacacarerererererererererererere CTGGGCATGCATGCTGCCACCTCACTCCCACTCTCTCTTATGAGCCTACTGGCCAT 489 GAAATACAAATATITAAAAATATAAATTITAAAAAACATTCTAAAGGTCATTCAGATCCT OCTCAGCTCCCTCCTCCACACATGTCTCAGTCTCACTTTCGACTTTGGCTTTTTCACTA Gaps 84; 69.3%; Score 795; DB 6; Length 1872; 85.7%; Pred. No. 7.4e-129; Live 0; Mismatches 90; Indels 8 Best Local Similarity 85.7 Matches 1043; Conservative 370 1183 549 608 1302 668 728 Query Match 430 848 셤 ò 유 셤 ઠે g 셤 셤 白 δ ઠે ठ 8 ò g 8 8 8 8 ર્જ g 8 8 8 음 중 음 8

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                                                1649
                                                                          CCATAAATATCTATTTAAATTTAAACTAATTATTTCAFATACTTTTTTGATGACGTGGAT 1027
                                                                                       1131
                                                                                                                                                                                       .530 CTGGGCATGCATGCCACCTCAGCTCCCACCTCTTCTCATTATGAGCCTACTGGCCAT 1589
                                                                                                                          ------ 1073
                                                                                                                                                   1710 GCATTGCCATCGTTGTTATTGTTAATTTTATTTATTATTTCTCCCTCAAATAAT 1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated cgd dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guetig D, Howe A, Mueller J;
P, Grabs G, Lesche R, Leu E;
Model F, Mueller V, Otto T, Pelet
                                           1590 GCACACTGCCACCTCCACTCTCACTTCCCATTGCTACCTGCCAAACCGCTTCTCT
                                                                                                                                                                            1074 AAAATGAAAGAAAAAGTTGGA--AAGATTTTGCATTGTTGTTGTTAAATAGAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                             Haematopoietic cell proliferation disorder related DNA sequence #386.
                                                                                                                                                                                                                                                                                                                                                                                                                    Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                                                                                                            1028 GCATTGCCATCGTTGTTTAATAATTGTTAATTTGGAGTT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 28; SEQ ID NO 386; 117pp; English.
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Olek A, Piepenbrock C, Adorjan
Lewin A, Lipscher E, Maier S,
Schwope I, Ziebarth H;
                                                                                                                                                                                                                                GAGTGATGGTTAATGCA 1148
                                                                                                                                                                                                                                            ВЪ
                                                                                                                                                                                                                                                                                                                       ABZ10246 standard; DNA; 8056
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                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG.
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                                                                           968
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                                                                                                                                                                                                                                                                                              RESULT 7
ABZ10246
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lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of hematopoietic cell proliferation disorder related sequences and their complements, and as primers for the amplification of haematopoietic cell proliferation disorder related bNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAACAATTTTGTTAAACATCTTATTAGAAACTTTTAGTTAAGTCTTGAAGTTAGAATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 TGAAATGTTTTGATATCATTAAATATAACACACACAAAAATACATCTAATTATAACAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATGTTATACATATTTTTTGTAAAACTTTAGAGTTTTTCAAAACATTCTAATACATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        478 TAGAGITITATAGAAATACAAATATITAAAAA----ATATAATITITAAAAAAACATICIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 AAAAAATGICCTTAICTCTTTGITTCCTAATAATAATAAGAGAGACTTAAACTTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 ACAAAAAAATTACACACAGAAAACACAATAAACCCACTACCGTCAGGTTATCATAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ъ,
                                                                                                                                                                                                                                                                                                                              Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                 Length 8056;
                                                                                                                                                                                                                                                                                                                                                                                                                                    0, Mismatches 325, Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    654 ATTAAATAAAAAGGGAAAATCAAATTAGAATTTTGATT 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haematopoietic cell proliferation disorder related
                                                                                                                                                                                                                                                                                                                                                                                 7.8%; Score 90; DB 7; 148.4%; Pred. No. 1.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1199/c
ABZ10199 Btandard; DNA; 3683
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 310; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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TTANACAAAAAATTACACACGAGAAACACAATAAACCCACTACCGTCAGGTTATCATA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expression cassette; promoter activity; suspensor cell; plant embryo; modulation of gene transcription; Scarlet runner bean; C541; plant; gene;
                                                                                                                  AGGATGAAATGITTTTGATATCATTAAACACACACACAAAAATACATCTAATTATAAC
                                                                                                                                                               414 AATATATGTTATACATATATTTTTGTAAAACTTAGAGTTTTTCAAAACATTCTAATACA
                                                                                                                                                                                                                                                                                                                 654 ATTARATARARARAGGGARARATCRARTTAGARTTTTTGATTCCCCACATGACACAACTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression cassette comprises promoters with basal promoter activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "C541 protein"
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3154. .3552
/*tag= a
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28-NOV-2000; 2000US-0253672P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-NOV-2001; 2001WO-US044737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2653 CTTTCCCAC 2645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phaseolus coccineus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders differentiating between haematopoietic cell proliferative disorders consisted with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated oped dinucleotides within the target nucleic acid. AB203861 to ABZ1118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention on be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute disorder haematopoietic cells; for differentiating between acute disorder haematopoietic cells, for differentiating between acute complements; and as primers for the determining the cytosine methylation state and/or single nucleotide sequences and their complements; and as primers for the complements and as primers for the complements and as primers for the sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between consubclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorder: The present method enables a highly specific classification of haematopoietic cell proliferative cell proliferative childs of haematopoietic cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell prolifera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
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                                                                                                                                                                                                                                                                                                                                                                                          Guetig D, Howe A, Mueller J;
P, Grabs G, Lesche R, Leu E;
Model F, Mueller V, Otto T, Pelet C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 ACAGITAACAAAACAAATTTATGITTCAITTGAGAITTAAGGAAGGTAAGGAAAAAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 ATTAAAAAAATGTCCTTATCTCTTTGTTTCTGTAATAATAATAATAAGAGACTTAAACTT
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                          gene therapy, lymphocytic leukaemia, acute myelogenous leukaemia,
cytosine methylation state, gene, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
Human; haematopoietic cell proliferation disorder; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3683;
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Best Local Similarity 46.6%; Pred. No. 4.4e-06;
Matches 312; Conservative 0; Mismatches 355; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 28; SEQ ID NO 339; 117pp; English
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Piepenbrock C, Adorjan
Lipscher E, Maier S,
                                                                                                                                                                                                                                                26-MAR-2002; 2002WO-BP003401.
                                                                                                                                                                                                                                                                                          26-MAR-2001; 2001US-0278333P
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Schwope I, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                              (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-018942/01.
                                                                                                                                             WO200277272-A2
                                                                                                   Homo sapiens
                                                                                                                                                                                              03-OCT-2002
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                                                                                         The present invention relates to expression cassettes comprising a promoter sequence and a promoter polynucleotide with basal promoter activity, where the promoter sequence is operably linked to a heterologous polynucleotide, and when the expression cassette is inserted into a plant, the heterologous polynucleotide is specifically expressed in a suspensor cell and/or basal region of a plant embryo. The invention also provides polynucleotide sequences encoding Scarlet runner bean (Phaseolus coccineus) 6564 and 6341 proteins for use in the expression cassettes of the invention. The expression cassettes comprising promoters and promoter control elements are useful for modulating transcription of genes in a plant suspensor cell and/or basal region of a plant embryo. The present sequence represents Scarlet runner bean C541 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1145 TACATOCTAAAGTOTTTCAGACCCTOTGACACATGT---ATCATOTGCTOCTATATGTGA 4201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                464 ITCTAATACATGATTTAGAGTTTATAGAAATACAAATATTTAAAAAATATTATAAAAA 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New transformed or transgenic soybeans plants or cells with an Arcelin-5 promoter, for use as an improved dietary source of protein for humans or animals, or for producing soybeans with important agricultural or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4262 TCCATAACATATTTAATTCATGCAAAAGAACCAGTCAAAGTAATCATTTATAAACAT 4319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arcelin-5; promoter; plant; transgenic; soybean; agriculture; nutrition; pharmaceutical; ds.
operably linked to a heterologous polymucleotide, useful for expression genes in suspensor cells in plants and/or basal region of plant embryo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1202 TACAGTCATCGCAGTTCACAAGATAACAAGAAAACCAAGGGTAAGCTAATGAAAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          644 AATATATACAATTAAATAAAAAGGGAAAATCAAATTAGAATTTTTGATTCCCCACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                            Sequence 4846 BP; 1894 A; 777 C; 753 G; 1415 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                    Length 4846;
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.4%; Score 85.2; DB 6; Length 4 Best Local Similarity 65.5%; Pred. No. 9.2e-06; Matches 156; Conservative 0; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oulmassov T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arcelin-5 promoter sequence fragment
                                                           Claim 25; Fig 4; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-DEC-2001; 2001WO-US047495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2000; 2000US-0255879P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABN83926 standard; DNA; 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RENE-) RENESSEN LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-508809/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dubois P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phaseolus vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200250295-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABN83926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
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임
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                                                                 The invention relates to a transformed soybean plant cell and transgenic soybean plant, both of which has a nuclet acid molecule comprising the phaseolus vulgaris exotic genotype 002711 Arcelin-5 promoter sequence. The transformed soybean plant cell and transgenic soybean plant are useful as an improved source of dietary protein for humans and livestock. These are also useful for producing soybean plants that exhibit important agricultural, nutritional or pharmaceutical properties. The current sequence represents an arcelin-5 promoter sequence fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pelet C;
                                                                                                                                                                                                                                                                                                                                                                              204 TCGTTGTTTAATAATTGTTAATTTGGAGTTGAATAATAAAATGAAAGAAAAAGGTTGGAA
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haematopoietic cell proliferation disorder related DNA sequence #240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Howe A, Mueller J;
G, Lesche R, Leu E;
Mueller V, Otto T,
                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                    7.4%; Score 85; DB 6; Length 288;
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                  Sequence 288 BP; 121 A; 26 C; 38 G; 103 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                  100.0%; Pred. No. 7.9e-06; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guetig D,
P, Grabs
Model F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 28; SEQ ID NO 240; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  1097 AGATTTTGCATTTGTTGTTATAA 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                   264 AGATTTTGCATTTGTTGTTATAA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berlin K, Braun A, Distler J,
Olek A, Piepenbrock C, Adorjan
Lewin A, Lipscher E, Maier S,
                                Example 1; Fig 1; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ10100 standard; DNA; 8056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2001; 2001US-0278333P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002; 2002WO-EP003401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                      Local Similarity 100.
nes 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olek A, Piepenbrock C,
Lewin A, Lipscher E, N
Schwope I, Ziebarth H;
nutritional properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-018942/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABZ10100;
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
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c dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118

C represent specifically claimed rucleotide sequences from the present
invention. Oligonucleotides from the present invention can be used: for
differentiating between healthy heamatopoietic cells and proliferative
C disorder haematopoietic cells; for differentiating between acute
Iymphocytic leukaemia and acute myelogenous leukaemia; as probes for
determining the cytosine methylation state and/or single nucleotide
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC mapification of haematopoietic cell proliferation disorder related DNA
sequences. The nucleotide sequences from the present invention can also
cc be used for detecting a predisposition to, differentiation between
CC be used for detecting a predisposition to, differentiation between
CC chaematopoietic cell proliferative disorders. The present method enables a
highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
Sequence BOS6 BP; 3711 A; 371 C; 371 G; 3603 T; O U; O Other;
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1639 AAITAAAAAAATTATTTAATTAATACGATAAAATTTFATTTTATTAAAATTATAAAA 1698 278 398 458 459 AAACATTCTAATACATGATTAGAGTTTATAGAAATACAAATATTTAAAAAATATTTT 518 519 AAAAAAACATTCT--AAAGTCATTCAGATCCTCTCACACCTGTGTGATCATTTAGTCATG 576 279 GTCTTGAAGTTAGAATTAAACAAAAAATTACACACGAGAAACACAAATAAACCCACTAC 338 100 AAGGAAGAAAAAAAATTAAAAAAAAATGTCCTTATCTCTTTGTTTCTGTAATAATATATA 159 TATATATATATATATACAATTAAATAAAAAGGGAAAATCAAATTAGAATTTTGATT 693 219 CAGAGACAAGATTTTCAAGAAACAATTTTGTTAAACATCTTATTAGAAACTTTTAGTTAA AGAGACTTAAACTTTTAATATA - ATAATTGTAATTAGGTTTTTCTAGTCATGAGCACCACT 399 ACATCTAATTATAACAATATATGTTATACATATATTTTTGTAAAAACTTAGAGTTTTTCA 7.4%; Score 85; DB 7; Length 8056; 49.7%; Pred. No. 1e-05; 0, Mismatches 295, Indels Local Similarity 49.7 les 297; Conservative 577 637 160 Query Match Best Loca Matches

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in present invention describes a meritod to describe and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a terget mucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinuclectides within the terget nucleic acid. AB209861 to AB21118 capresent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haemaclopicitic cells and proliferative disorder haematopoietic cells, for differentiating between a probes for determining the dytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the cylonophisms (SNPs) of haematopoietic cell proliferation disorder related camplification of haematopoietic cell proliferation disorder related sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, disgnosis, prognosis, treatment and/or monitoring of subclasses, disgnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables disorders allowing for improved and informed treatment of patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent the distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>rripripripariarpripripricampripripaaatorpaaaatoaaapuntutot</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATCTCTTTGTTATAATAATATATAAGAGACTTAAAACTTTTAATAATAATTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTAGGTTTTCTAGTCATGAGCACCACTCAGAGACAAGATTTCAAGAAAAAAATTTTGTT
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                   Human, haematopoietic cell proliferation disorder; cytostatic; gene therapy, lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                       Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J,
Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E,
Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.4%; Score 84.8; DB 7; Length 8056; 18.7%; Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the present invention describes a method for detecting and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 302; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 28; SEQ ID NO 386; 117pp; English.
                                                                                                                                                                                                                                                    26-MAR-2002; 2002WO-EP003401.
                                                                                                                                                                                                                                                                                                   26-MAR-2001; 2001US-0278333P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 48.7%;
Matches 290; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           Lewin A, Lipscher E, 1
Schwope I, Ziebarth E;
                                                                                                                                                                                                                                                                                                                                                (BPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-018942/01.
                                                                                                                                                           WO200277272-A2.
                                                                                                                 Homo sapiens.
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1062 -----GAGTTGAATAATAAAGAAAAAG 1090
                                                           126 ATTGCCATCGTTGCTTAATTCTTATTTTTTTTTTTTCTCCTCAAATAATATTAC 185
                                                                                                      ----ACTITITIGATGACGTGGATGC
           Human immune system associated gene SEQ ID NO: 1549.
                                            .030 ATTGCCATCGTTGTTTAATAATTGTTAATTTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berlin
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01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                     ABL33576 standard; DNA; 5925
                                                                                                                                                                                                                                                26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methylation.
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                                                                                                                              1001
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ABL33576/c
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   486
                                                                                                                                                   546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New kidney bean gene encoding lectin-like protein - for the production of insect-resistant crop plants.
                                                                 429
                                                                                                                                                                                             547 CTCTCACACCTGTGTGATCATTTAGTCATGTAGTACTACAATCATTGTAGTTCACAACA 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The DNA encodes a lectin-like protein isolated from kidney bean var. Kentucky Wonder. The gene provides insect-resistance to crop plants, and is also useful as a DNA marker in gene and genomic analysis
                                                                                                                                                                                                                                                           1680 AATAAAATITTAICATATIAATTAAATAAITITITITITAATITITAAATITCATITA 1625
                                                                                                                                                  487 TAGAAATACAAATATTTAAAAAATATATATATAAAAAAACATTCTAAAAGTCATTCAGATC
                        310 ACACACGAGAAACACAATAAACCCACTACCGTCAGGTTATCATAAGGATGAAATGTTTTG
                                             370 ATATCATTAAATATAACACACACAAAAATACATCTAATTATAACAATATATGTTATACAT
                                                                                                           430 ATAITITIGIAAAAACITAGAGITITICAAAACAIICIAAIACAIGAITAGAGI---ITA
                                                                                                                                                                                                                                      607 GAGTAAATAAATAAGGATAAACTAGGGAATATATATAATATATACAATTAAATAA 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   ectin-like; kidney bean; insect resistance; genomic analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 84.4; DB 2; Length 1211;
Pred. No. 1.1e-05;
0; Mismatches 31; Indels 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1211 BP; 344 A; 322 C; 203 G; 342 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Fig 1-3; 6pp; Japanese.
                                                                                                                                                                                                                                                                                                                 AAQ94051 standard; DNA; 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93JP-00305988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.4%;
Best Local Similarity 67.1%;
Matches 200; Conservative
                                                                                                                                                                                                                                                                                                                                                                              Kidney bean lectin-like gene
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                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                   Phaseolus vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                               DNA marker; ss.
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AAQ94051
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                                         antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
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system disease; cytosine methylation; antiasthmatic;
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7.3%; Score 83.4; DB 6; Length 5
Best Local Similarity 49.5%; Pred. No. 1.9e-05;
Matches 351; Conservative 0; Mismatches 351; Indels
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                                                                                                                                                                                                                                                                                                        426
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67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            547 CTCTCACACCTGTGTGATCATTTAGTCATGTAGTAGTACAATCATTGTAGTTCACAACA
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                                               ATABATATATABATACTATATTAA-AAATATAAACAAAATACTATAAAAACACAAT
                                                                                                 128 CCTTATCTCTTTGTTTCTGTAATAATAATAAGAGACTTAAAACTTTTAATAATAATT
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ir suppressor gene; oncogene; antitumour; cytostatic; cancer; dinuclectide; single-nucleotide polymorphism; SNP;
                                                                                Tumour suppressor gene derived chemically modified sequence #472
                   BP
                                                                                                         Human; tumour suppressor gene;
                    AAS46748 standard; DNA; 26997
                                                                                                                                                                                                                                       15-MAR-2000; 2000DE-01013847
                                                                                                                                                                                                                  15-MAR-2001; 2001WO-EP002955
                                                               (first entry)
                                                                                                                    tumour; CpG dinucleotide;
cytosine methylation; ds.
                                                                                                                                                                         W0200168912-A2
                                                              18-DEC-2001
                                                                                                                                                    Homo sapiens
                                                                                                                                                                                             20-SEP-2001
                                         AAS46748;
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6736

TTTTGATATCATTAAATATAACACACACAAAAATACATCTAATTATAACAATATATGTTA 424

6735

365

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TGTCCTTATCTCTTTTCTGTAATAATATATAAGAGACTTAAACTTTTAATATATA 184

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6975 AACTAATATCTATAAATAACAAATAAACCTAAAAACTAAAATATAAATTAAAATAAC

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7795 aaataaaaaaatariracaaactafacaffraacaaaaakcraatarccaaaarccac AAATTACACAGAAAACACAATAAACCCACTACCGTCAGGTTATCATAAGGATGAAATG 

245 TITGITAAACAICITAITAGAAACITITAGITAAGICITGAAGITAAGAATTAAACAAAA

185 ATTGTAATTAGGTTTTCTAGTCATGAGCACCACTCAGAGACAAGATTTCAAGAAAACAAT

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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes bisulphite, of genes associated with tumour suppression and oncogenes complementary to (Ss). The nucleic acid may be a peptide nucleic acid complementary to (Ss). The nucleic acid may be a peptide nucleic acid oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single cucleotide polymorphisms and also to be used in an array for analysing diseases associated with CG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters may be compared to another set of patients. The present sequence is one of the S13 genomic sequences of the citients. The present sequence is one of the S13 genomic sequences of patients. The present sequence is one of the S13 genomic sequences of the corresponding odd numbered sequence (e.g. ID 2 and ID), ID 536 and ID corresponding odd numbered sequence (e.g. ID 2 and ID), ID 536 and ID corresponding odd numbered parameters sequence is missing). Note: The sequence data for this patent did not form part of the printed sequence in the parameters sequence is missing). Note: The sequence is not of the sequence of the sequence data for this patent did not form part of the printed in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6976
                                                                                                                                                                                                                                                                                                        Pragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCTATCTTCCCAACTCCTATTTACTCTTTAATACCACATATTACATAAAACTATCAA
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7.2%; Score 83; DB 4; Length 269
Best Local Similarity 45.1%; Pred. No. 2.5e-05;
Matches 308; Conservative 0; Mismatches 375; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 472; 27pp; English
                                                                                                                                                                                                Berlin K;
06-APR-2000; 2000DB-01019058.
07-APR-2000; 2000DB-01019173.
30-4UN-2000; 2000DB-01035529.
01-SEP-2000; 2000DB-01043826.
                                                                                                                                                                                              Piepenbrock C,
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6435 CATABABARCTARTACARCCACTATABABACTACTACCACTATABABABACARTATABABA 6376
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                                                                                                   545 TCCTCTCACACCTGTGTGATCATTTAGTCATGTAGTACTACAATCATTGTAGTTCACAA 604
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Search completed: June 2, 2004, 02:24:19 Job time : 546 secs

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2, 2004, 02:26:24 ; Search time 4650 Seconds (without alignments) 10700.603 Million cell updates/sec
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GenCore version.5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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1148
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Perfect score:
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the number of results predicted by chance to have a (B) Š. Pred.

PAT 15-JUL-2002

linear

DNA

1148 bp Sequence 1 from Patent WO0250295. AX463281.1 GI:21886232

RESULT 1
Ax463281
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

ALIGNMENTS

Phaseolus vulgaris Phaseolus vulgaris Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosiás; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.

Oulmassov, T., Wang, Q., Dubois, P. and Liang, J.

REFERENCE AUTHORS

AX463281 Sequence
AX463282 Sequence
AX463292 Sequence
AX63292 Sequence
AX63293 Sequence
AX63293 Sequence
AX65293 Sequence
AX65291 Sequence
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AX65291 Sequence
AX65291 Phaseolus
AC01261 P. Vulgaris
M69319 Phaseolus
B09281 DNA encodins
AC0288 Phaseolus
AC015539 Homo sapi
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AC01553 Pulgaris
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AC01329 Homo sapi
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AC013281 Homo sapi Mus muscu Dictyoste Caenorhab score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. AP001398 AC006882 AC073681 BX511263 AC073671 AV159038 AL022288 AL022288 AC145619 AP000022 I SUMMARIES AC073567 AC016419 AC128028 AC125570 AX463290 AX463290 AX463289 PVDLEC2A PVDLEC2B AC024825 AL450352 AC117426 AC073207 AL929216 AC001398 AC006882 AC006882 PVDLEC1 PHVDLECA AC096559 AC128689 AC015539 图 2.4 68875 2.4 123318 2.4 174569 2.4 174569 2.4 174569 2.4 2764954 2.3 316 2.3 188 2.3 188 2.3 1861 2.1 16609 2.1 16609 2.1 16609 2.1 16609 2.1 17483 2.1 18762 2.1 18752 2.1 18752 2.1 18752 2.1 234679 2.1 234679 2.1 234679 Query Match Length 100.0 100.0 97.7 91.1 Score Result No. 189 P υυυ

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Phaseolus vulgaris
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Pabales; Pabaceae; Papilionoideae; Phaseoleae;
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AUTHORS TITLE JOURNAL	Oulmassov, T., Wang, Q.; Arcelin-5 promoter and Patent: WO 0250295-A 2	<pre>Dubois, P. and Liang, J. uses thereof 27-JUN-2002;</pre>
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/db_xref="G1:3451282"
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FINNARDFHKYNGREKTDVQLTTYDSSNNDLAFVFLHFTVSOVKCSVGATVHLEKEVDEN
VSVGFSATGGLTEDTTETHDVLSWSFSSKFRNKLSNILLINNIL"
                                                                                                                  Goossens, A.
Direct Submission
Submitted (01-AUG-1995) Goossens A., Universiteit Gent,
Laboratorium Genetika, K.L.Ledeganckstraat 35, Gent, Belgium, 9000
Revised by [4]
4 (bases 1 to 3900)
                                                                                                                                                                                        Direct Submission
Submitted (13-AUG-1998) Goossens A., Universiteit Gent,
Laboratorium Genetika, K.L.Ledeganckstraat 35, Gent, Belgium, 9000
On Aug 25, 1998 this sequence version replaced gi:929816.
Location/Qualifiers
                                         Goossens, A., Ardiles Diaz, W., De Keyser, A., Van Montagu, M. and
                                                      Angenon, G.
Nucleotide sequence of an arcelin5-I genomic clone from wild
                                                                                                                                                                                                                                               Phaseolus vulgaris
Plant Physiol. 109, 722-722 (1995)
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1898. .2617
/gene="arc5-1"
/product="arcelin 5a"
/citation=[1]
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/evidence=experimental
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Phaseolus vulgaris
Phaseolus vulgaris
Bubryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus.
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Phaseolus vulgaris arcelin 5c gene, complete cds
                                                                                                                             Oulmassov, T., Wang, O., Dubois, P. and Liang, J. Arcelin-5 promoter and uses thereof
Patent: WO 0250295-A 12 27-JUN-2002;
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                                                                                                                                                                                                                                                                                                                            9.3%; Score 107; DB 6; 1
100.0%; Pred. No. 2.2e-43;
ive 0; Mismatches 0;
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100.0%; Pred. No. 5.6e-32;
tive 0; Mismatches 0;
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/organism="phaseolus vulgaris"
/mol type="unassigned DNA"
/db_xref="taxon:3885"
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/organism="phaseolus vulgaris"
/mol_type="unassigned DNA"
/db_xref="taxon:3885"
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Sequence 11 from Patent W00250295.
AX463291 GI:21886242
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Best Local Similarity 100.
Matches 107; Conservative
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Best Local S
Matches 85
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 1514 GACACCACTGGGCATGCTACCACCTCAGCTCCCACCTCTTCTCATTATGAGCCTAC 1573
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Phaseolus vulgaris
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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Best Local Similarity 100.0%; Pred. No. 2.2e-43;
Matches 107; Conservative 0; Mismatches 0; Indels
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Arcelin-5 promoter and uses thereof
Patent: WO 0250295-A 13 27-JUN-2002;
PATESSEN L.C. (US)
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/organism="Phaseolus vulgaris"
/mol_type="unassigned DNA"
/db_xref="taxon:3885"
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AX463293.1 GI:21886244
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Sequence 12 from Patent WO0250295.
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AX463293
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Length 288;

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/db_xref="G0A:PROT:P15231"
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/db_xref="SWISS-PROT:P15231"
/db_xref
BMBO J. 5, 3075-3082 (1986)
See also «Kowf660» for dlec1 gene (pseudogene).
Several inverted repeats are described in the 5' upstream region of the PHA coding region.
2 pot. glycosylation sites are found at the AA residues 33 and 92.
Pot. glycosylation sites are found (with respect to mRNA levels in normal cultivars); a 100bp deletion between pos. 501 and 502 (compared to dlec1, diec2 and PdLec1) containing a large tandem repeat may be responsible for the low level of expression of PdIec2.
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Hoffman, L.M., Ma, Y. and Barker, R.F.
Molecular cloning of Phaseolus vulgaris lectin mRNA and use of cDNA as a probe to estimate lectin transcript levels in various tissues Nucleic Acids Res. 10 (23), 7819-7828 (1982)
68971694
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/note="unnamed protein product; precursor polypeptide (AA
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Phaseolus vulgaris
Bukaryota, Viridlantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Pabales; Pabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:1885"
/tissue_type="young leaves (greenhouse)."
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/product="mature PHA (AA 1-252)"
1691. .1699
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100.0%; Pred. No. 8.9e-22;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                              /organism="Phaseolus vulgaris"
/mol_type="genomic DNA"
/strain="Pinto UII11"
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/protein_id="AAP23725.1"
/protein_id="G1:6684725.1"
/t znnslation="WASSMLLSLELUTLITHANSATETSFNFTSFHPDDPKLMLQGD
AT1STKGQLLLTSYYELSRUDSLGRALYSDPTQIKDNNNVASFDTKFTFIIRPETNGN
SAYGLAFALVPVGSKEPKGROPYLGIFNDTTPERDSARYNVENTLRNRIDIDVNAIKP
YANDKCDFHKNYGERTDVQITYDSSKNDLAFTVSQVKGSVSATVQLEKEVNEWN
SVQRSDATSGLTENTFFHDVLSWSFSSKRRNKLSNILLANIL"
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glycoprotein: Pollec2 gene; phytohemagglutinin;
phytohemagglutinin-L; signal peptide.
phytohemagglutinin-L; signal peptide.
Phaseolus vulgaris
Phaseolus vulgaris
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus.
                                                                                                                              Phaseolus vulgaris
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus.
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Submitted (07-OCT-1999) Embrapa/Cenargen, SAIN-Parque Rural-Final
W5 Norte, Brasilia, DF 70770-900, Brazil
Location/Qualifiers
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Molecular analysis of two phytohemagglutinin genes and their
expression in Phaseolus vulgaris cv. Pinto, a lectin-deficient
cultivar of the bean
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P. vulgaris cv.Pinto Pdlec2 gene for phytohemagglutinin (PHA)
X04659
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Molecular characterization of a new arcelin-5 gene
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100.0%; Pred. No. 7.7e-24;
ative 0; Mismatches 0;
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/mol type="genomic DNA"
/cultivar="G02771"
/db_xref="taxon:3885"
/clone="plG53"
/tissue_type="leaf"
<603. >1385
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                                            GI:6684755
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Matches 69; Conserv
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Best Local Similarity 100.0
Matches 48; Conservative
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PVPDLEC1
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265. .1005
//note="lectin prepeptide"
//note="lectin prepeptide"
//codon_start=1
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//protesh_d="GI:169355"
//db_xref="GI:169355"
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//translation="MIMASSKILESHALFLALLSHANSATETSFIIDAFNKTNLILQGD
//translation="Mimass"
//db_vrspringhtshalflation="Mimass"

//db_vrspring
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LSWSFSSKFINLKDQKSERSNIVLNKIL"
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arcelin; lectin-like seed protein.
Phaseolus vulgaris
Phaseolus vulgaris
Phaseolus vulgaris
Sparatophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Anthony, J.L., Vonder Haar, R.A. and Hall, T.C.
Nuclectide sequence of a genomic clone encoding arcelin, a lectin-like seed protein from Phaseolus
Plant Physiol. 97, 839-440 (1991)
Original source text: Phaseolus vulgaris (library: Lambda Zap II)
                                                    Structure of a chromosomal Phaseolus vulgaris lectin gene and its
                                                                                                                                                                                                                                                                             CAT and TATA boxes are located at positions 165-169 and 226-231 respectively. Two tandem poyadenylation signals are present at position 1084-1033.
A magnetic tage of this sequence and a draft entry were kindly provided by L.M.Meffman (23-OCT-1985).
                                                                                                                                                                                                     Original source text: P.vulgaris cv. Tendergreen DNA, clone
p-lambda-lec5.7 [2]; and cotyledon, cDNA to mRNA, clone pPVL134
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/organism="Phaseolus vulgaris"
/mol_type="genomic DNA"
/db_xref="taxon:3885"
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/mol_type="genomic DNA"
/db_xref="taxon:3885"
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100.0%; Pred. No. 1.5e-1
ive 0; Mismatches
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/note="lectin signal peptide"
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2 (bases 1 to 1689)
Hoffman, L.M.
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SYGLARALVPVGSREPGLKGRYLGLEPRTTVNDVDEAHTVANVPLDFTVSRNFIEIDVNSIRPI
ATBSCHYGENNGERARURITYDSPRADLRVSLLYPSSEEKCHVSATVPLEKEVBDWVS
VGFSATSGSKKETTETHNVLSWSFSSNFINFKKKSERSNILLNKIL"
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X04660.1 GI:21020
X04660.1 GI:2020

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Pabaceae; Papilionoideae; Phaseoleae;
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/mol_type="genomic DNA"
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/tisue type="young leaves (greenhouse)."
665. 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1068 AATAATAAAATGAAAAAAAAGTTGGAAAGATTTTGCATTTGTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.2%; Score 48; DB 8; Length 456
100.0%; Pred. No. 4.6e-13;
tive 0; Mismatches 0; Indels
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3375. ,4172
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                                                                                                                                                                                                                                   /product="arcelin"
                                                                                                                                                                                                                  codon_start=1
                                                                        3332. .3338
/gene="arc"
3361. .3364
/gene="arc"
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AP255723
AP255723.1 GI:8050712
                  708. .866

Anote="unnamed protein product; pseudogene region"

/codon grart=1
/protein id="CAA28363.1"
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/db_xref="RMFEMBL:CAA28363"
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bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus:
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/note="tt is tct in Pdlec2 (c deletion, causing a frame
shift mutation)"
1620. .1635
/note="put. polyA signal"
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Gerhardt,I.R., Pappas,G., Chrispeels,M.J. and Grossi de Sa,M.F.
Direct Submission
Submitted (13.APR-2000) Biotechnology, Embrapa-Cenargen, SAIN
Parque Rural- Final W5 Norte, CP 02372, Brasilia, DF 70 770-900,
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4.0%; Score 46; DB 8; Length 1768;
Best Local Similarity 100.0%; Pred. No. 5.3e-12;
Matches 46; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                       Match 3.7%; Score 42; DB 8; Length 1852; Local Similarity 100.0%; Pred. No. 6.1e-10; es 42; Conservative 0; Mismatches 0; Indels
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DNA enccding lectin-like protein of kidney bean.
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|db_xref="taxon:3885"
/note="put. TATA-box"
708. .866
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/gene="ARLS-IV"
/pseudo
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JP 1995132092-A/1.
unidentified
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unclassified.
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NORTH SUISANSYO NORYO SEREUTEU SHIGEN KENKYUSHO

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OS Phaseolus Sp. (kidney bean)

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CC 120115/09/C120112//C07K14/42, (C12N1/21,C12R1:19); CC

CC 120105/09/C120112//C07K14/42, (C12N1/21,C12R1:19); CC

CC 120105/09/C12011//C07K14/42, (C12N1/21,C12R1:19); CC

AUTI-Sense: No;

CC 120105/09/C12011//C07K14/42, (C12N1/21,19); CC

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Sequence 64, Appl
Sequence 19, Appl
Sequence 87, Appl
Sequence 87, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 213, Appl
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Sequence 213, Appl
Sequence 214, Appl
Sequence 216, Appli
Sequence 182, Appl
Sequence 182, Appl
Sequence 182, Appl
Sequence 16, Appli
Sequence 1, Appli
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Sequence 21, Appli
Sequence 31, Appli
                                                                                    June 2, 2004, 03:34:13; Search time 108 Seconds (without alignments) 5898.922 Million cell updates/sec
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
   /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-071-0358-19
US-09-071-0358-19
US-09-071-035-87
US-08-071-035-85
US-08-104-0728-6
US-08-351-413-7
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US-09-539-601-45
US-09-539-601-45
US-09-539-601-45
US-09-539-601-50
US-09-539-601-50
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                                                                                                                                                                                                                                                                     682709 seqs, 277475446 residues
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                                                            - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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Query
Score Match Length DB ID
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Maximum DB seq length: 200000000
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1148
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Perfect score:
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424 4 US-09-643-597-157 424 4 US-09-480-644-157 424 4 US-09-524-6154-157 424 4 US-09-606-4218-157 424 4 US-09-606-4218-157 424 4 US-09-221-107-157 427 4 US-09-221-107-157 487 4 US-09-713-550-176 487 4 US-09-713-550-176 487 4 US-09-596-1718-937 846 4 US-09-556-1718-937 846 4 US-09-134-0012-1926 916 3 US-09-294-012-29 1001 4 US-09-541-638-161 1072 1 US-09-641-638-161 1072 1 US-09-9175-096-1 1172 4 US-09-598-4012-90 1172 4 US-09-598-4012-90 1072 1 US-09-598-4012-90 1172 1 US-08-175-096-1 1172 1 US-09-598-4012-90	ALIGNMENTS	DLT 1 08-976-259-64 08-976-259-64 acquence 64, Application US/08976259 atent No. 6316609 BENERAL INFORMATION: APPLICANT: Dillon, Patrick J. APPLICANT: Choi, Gil H. APPLICANT: Welch, Rodney A. TITLE OF INVENTION: Nucleotide Sequence of Escherichia atent No. 6316609 NUMBER OF SEQUENCES: 142 CORRESPONDENCE ADDRESS: STREET: 1100 New York Resiler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Resiler, Goldstein & Fox P.L.L.C. STREET: USA SEQUENCES: 1846/33 CCOUNTY: Washington STATE: CCOUNTY: USA CCOUNTY: USA CCOUNTY: Hashington STATE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 COUNTY: HP Vectra 486/33 COUNTY: HP Vectra 486/33 COUNTY: APPLICATION NUMBER: US/08/976,259 FILING DATE: Herewith CLASSIFICATION NUMBER: US/08/976,259 FILING APPLICATION NUMBER: 356 RIOR APPLICATION NUMBER: 36.688 REFERENCE/DOCKET	1.8%; Score 21; DB 4; Length 7 larity 100.0%; Pred. No. 2.7; Conservative 0; Mismatches 0; Indel massabasamemens 20
		SULT 1: -08-976-259-64  -08-976-259-64  Sequence 64, Application U Patent No. 631669  GENERAL INFORMATION: Pat APPLICANT: Choi, Gil H APPLICANT: Choi, Gil H APPLICANT: Choi, Gil H APPLICANT: Melch, Rodn TITLE OF INVENTION: Nu Patent No. 631669  NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS: ADDRESSEE: Sterne, K STREET: 1100 New YOF CITY: Washington CITY: Washington CITY: Washington STATE: DC COMUTRY: USA  ZIP: 20005-3934  COMUTRY: USA COMUTRE READABLE FORM: MEDIUM TYPE: DISKETT OMPUTER: HP VECTRA OMPUTER READABLE FORM: MEDIUM TYPE: DISKETT OMPUTER: HP VECTRA OMPUTER: APPLICATION DATA: APPLICATION NUMBER: PILING DATE: HEFWRIT REGISTRATION NUMBER: ATTORNEY/AGENT INFORMAT NAME: STEFF, ENTOR TELEPHONE: (202) 371-2 INFORMATION FOR SEQ ID NO SEQUENCE CHARACTERISTIC LENGTH: 7430 base pa TYPE: NUCLEIC GOUL STRANDENNESS: GOULIEC TOPOLOGY: linear	Similarity 21; Conser
		-64 53.4 Applica 63.4 Applica 11. Dillo 12. Dillo 13.4 Applica 63.6 Applica 63.6 Applica 63.6 Applica 63.6 Applica 63.6 Applica 63.6 Applica 63.6 Applica 63.6 Applica 63.6 Applica 64.6 Applica 65.6 Ap	Simi 1;
		176-259-64 hnce 64, Appl. hnce 64, A	Match ocal s 2
22000000000000000000000000000000000000		SULT 1  -08-976-259-64  -08-976-259-64  Sequence 64, Applia  Patent No. 6316609  GENERAL INFORMATI  APPLICANT: Dil APPLICANT: Cho APPLICANT: Well TITLE OF INVENT  ADDRESSEE: SOUE CORRESPONDENCE. ADDRESSEE: LIOO CITY: Washin STATE: LOC COUNTRY: USA COMPUTER: HP OPERATING SYS SOFTWARE: AS COMPUTER READAB MEDIUM TYPE: COMPUTER: HP OPERATING SYS SOFTWARE: AS CURRENT APPLICATION N FILING DATE: CLASSIFICATION N FILING DATE: CLASSIFICATION N FILING APPLICATION APPLICATION N FILING DATE: CLASSIFICATION ATTORNEY/AGENT NAME: SCEFFE REGISTRAATION TELEPHONE: (20 INFORMATION FOR SISCUENCE CHARAC LENGTH: 7430 INFORMATION FOR SISCUENCE CHARAC LENGTH: 7430 INFORMATION FOR SISCUENCE CHARAC INFORMATION	Query Match Best Local Matches 2
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Sequence 87, Application US/09071035
Sequence 87, Application US/09071035
Sentence 81, Application:
APPLICANT: GII H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
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J Sequence 19, Application US/09807258
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J Sequence 19, Application US/09807258
J SEQUENCE 10, E670166
J GENERAL INFORMATION:
J TITLE OF INVALOR ARTHOROGY Protein Disulfide Isomerases
J TILE REFERENCE: BB-1253 PCT
J CURRENT APPLICATION NUMBER: US/09/807,258
J CURRENT FILING DATE: 2001-06-11
J PRIOR APPLICATION NUMBER: 60/104,376
J PRIOR APPLICATION NUMBER: 60/104,376
J PRIOR PILING DATE: 1998-10-15
J NUMBER OF SEQ ID NOS: 32
J SOFTWARE: Microsoft Office 97
J SEQ ID NO 19
J SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 1.7%; Score 20; DB 4; Length 802; Best Local Similarity 100.0%; Pred. No. 8.3; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
7289 ATTTAAAAAATATAATTTTAA 7309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1070 TAATAAATGAAAGAAAAA 1089
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME:
REFERENCE/DOCKET NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB365
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 87:
SEGUENCE CHERACTERISTICS:
LENGTH: 1597 DASE PAIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1597 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: ,
US-09-071-035-87
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US-09-071-035-87
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pactor of 2844, Application US/09134000C

pactor of 2844, Application US/09134000C

patent No. 6617156

GENERAL INFORMATION:

TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: WIGHER OF SECONDESTICS AND THERAPEUTICS

TITLE OF INVENTION: WIGHER: US/09/134,000C

CURRENT APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

NUMBER: OF SEQ ID NOS: 6612

SOFTWARE: Patentin version 3.1

SEQ ID NO 2844

LENGRIP 1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-05-071-035-85

### Sequence 85, Application US/09071035

### Patent No. 6448043

### Patent No. 6448043

### GENERAL INFORMATION:

### APPLICANT: Gil H. Choi

### TITLE OF INVENTION:

### NUMBER OF SEQUENCES:

### ADDRESSES: Human Genome Sciences, Inc.

### STERET: 9410 Key West Avenue

### CITY: Rockville

### STATE: Maryland

### CONNTRY: USA
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                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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100.0%; Pred. No. 8.1;
tive 0; Mismatches 0; Indels
  Score 20; DB 4; Length 1597;
Pred. No. 8.1;
                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486633
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
Query Match 1.7%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 8.1 Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1189 AAAATCAAATTAGAATTTT 1208
                                                                                                                                         1112 AAAATCAAATTAGAATTITT 1131
                                                                                              670 AAAATCAAATTAGAATTITT 689
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Matches 20, Conserva
                                                                                                                                                                                                                     RESULT 4
US-09-134-000C-2844
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LENGTH: 3627 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
APPLICANT: Michiels, Frank
APPLICANT: Michiels, Frank
APPLICANT: Morioka, Sinji
APPLICANT: Scheirlinck, Trees
APPLICANT: Scheirlinck, Trees
APPLICANT: Scheirlinck, Trees
APPLICANT: Morioka, Stamen-specific Promoters from Rice
ITTLE OF INVENTION: Stamen-specific Promoters from Rice
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5639948west Center
CITY: Minneapolis
                                                                                                                                                                                                                     Query Match
1.7%; Score 20; DB 4; Length 1680;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USAS

ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/104,072B
FILING DATE: 05-AUG-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: W0 9200272
FILING DATE: 06-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91403352.7
FILING DATE: 06-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 9140280.3
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 9140318.1
FILING DATE: 08-FEB-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,948
FILING DATE: 08-FEB-1991
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 8076.93USWO
TELECOMOTORICATION NUMBER: 36,948
REFERENCE (ACAPANTION: 1FORMATION:
TELECOMOTORICATION NUMBER: 36,948
REFERENCE (ACAPANTION: 1FORMATION:
TELECOMOTORICATION NUMBER: 30,948
TELEFRAX: 612-332-59081
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
I.FNGTH: 3627 base pairs
                                                                                                                                                                                                                                                                                                                                                                              1192 AAAATCAAATTAGAATTTTT 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08104072B Patent No. 5639948
                                                                                                                                                                                                                                                                                                                               670 AAAATCAAATTAGAATTTT 689
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                         LENGTH: 1680 base pairs
TYPE: nucleic acid
TYPE: TOPOLOGY: linear
US-09-071-035-85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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MOLECULE TYPE: I
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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US-08-104-072B-6/c
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NAME/KEY.

INDESTRICTION: 1.0.7845

OUTER INPOSMATION: Authorion= "sequence comprising or THE INPOSMATION: Author-specific FT72 promoter"

NAME/KEY: TAYLA. Signal INPOSMATION: Author-specific FT72 promoter"

NAME/KEY: TAYLA. Signal INPOSMATION: Aid-sequence comprising or THER INPOSMATION: Aid-sequence or THER INPOSMATION: Aid-sequence or THER INPOSMATION: Aid-sequence or THER INPOSMATION: Aid-sequence or THER INPOSMATION: Aid-sequence or THER INPOSMATION: Aid-sequence or THER INPOSMATION: TT7 gene or THER INPOSMATION: TT7 gene or THER INPOSMATION: TT7 gene or THER INPOSMATION: TT7 gene or THER INPOSMATION: TT7 gene or THER INPOSMATION: TT7 gene or THER INPOSMATION: TT7 gene or THER INPOSMATION: TT7 gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or Tht gene or THT gene or Tht gene or THT gene or THT gene or Tht gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene or THT gene o
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RESULT 9
US-10-027-983-11/c
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| NAME/KEY: -
| LOCATION: 2846..2848 |
| OTHER INFORMATION: /label= ATG |
| OTHER INFORMATION: /note= "ATG start of translation of rice T72 gene"
                                                                                                                                                                                                                               /note= "sequence comprising anther specific promoter PT72"
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GENERAL INCORMATION:
APPLICANT: Williams, Mark
APPLICANT: Leemans, Jan
TITLE OF INVENTOR: Maintenance of male-sterile plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 2046
COMPUTER FALDABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3627;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "transcription initiation
determined by primer extension"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.7%; Score 20; DB 1; Best Local Similarity 100.0%; Pred. No. 7.9; Matches 20; Conservative 0; Mismatches (
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LOCATION: 2733..2739
OTHER INFORMATION: /label= TATA
OTHER INFORMATION: /note= "TATA Box"
NAME/KEY: -
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APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-UTN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
                                                                                                                                                                                                                      /label= PT72
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                             ORGANISM: Oryza sativa
STRAIN: Akihikari
                                                                                                                                                                          LOCATION: 2765
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                           ORIGINAL SOURCE:
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patent No. 6617462
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION
CURRENT APPLICATION NUMBER: US/10/027,983
CURRENT FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 11
LENGTH: 392000
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NAME/KEY:
NAME/KEY:
OCHRENINON: 2846..2848
OTHER INFORMATION: /label= ATG
OTHER INFORMATION: /note= "ATG start of translation of rice T72 gene"
US-09-025-583-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "sequence comprising anther specific promoter PT72"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
1.7%; Score 20; DB 2;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Svensson, Leonard R.
REGISTRAFION NUMBER: 30,330
REMERNICE/DOCKET NUMBER: 2121-102PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAK: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= PT72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1071 AATAAAATGAAAGAAAAAG 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           991 AATAAATGAAAGAAAAAG 972
                                                                                              TELEPAX: (703) 205-8050
TELERAX: 248345
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3627 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPPOLGGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                             HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
GRGANISM: Oryza sativa
STRAIN: Akihikari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: 137740
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 137742
                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY:
LOCATION:
LOCATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: -
LOCATION: 2765
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INPORMATION: unknown
OTHER INPORMATION: unknown
OTHER INPORMATION: unknown
NAME/KEY: unsure
LOCATION: 145507
OTHER INPORMATION: unknown
NAME/KEY: unsure
LOCATION: 145507
OTHER INPORMATION: unknown
NAME/KEY: unsure
LOCATION: 145507
OTHER INPORMATION: unknown
NAME/KEY: unsure
LOCATION: 14567)...(14436)
OTHER INPORMATION: un = A,T,C or G
NAME/KEY: unsure
LOCATION: 14567)...(14436)
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NAME/KEY: unsure
LOCATION: 14567)...(14436)
OTHER INPORMATION: un = A,T,C or G
NAME/KEY: unsure
LOCATION: (146524)...(148523)
OTHER INPORMATION: un = A,T,C or G
NAME/KEY: unsure
LOCATION: (16524)...(13823)
OTHER INPORMATION: un = A,T,C or G
NAME/KEY: unsure
LOCATION: (16524)...(13823)
OTHER INPORMATION: un = A,T,C or G
NAME/KEY: unsure
LOCATION: (20254)...(202870)
OTHER INPORMATION: un = A,T,C or G
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OTHER INPORMATION: un = A,T,C or G
NAME/KEY: unsure
LOCATION: (202560)...(222489)
OTHER INPORMATION: un = A,T,C or G
NAME/KEY: unisc feature
LOCATION: (222560)...(222489)
OTHER INPORMATION: un = A,T,C or G
NAME/KEY: unisc feature
LOCATION: (222561)...(22386)
OTHER INPORMATION: un = A,T,C or G
NAME/KEY: unisc feature
LOCATION: (222561)...(223889)
OTHER INPORMATION: un = A,T,C or G
NAME/KEY: unisc feature
LOCATION: (222529)...(22389)
OTHER INPORMATION: un = A,T,C or G
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LOCATION: (222529)...(22389)
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NAME/KEY: unisc feature
LOCATION: (222529)...(223869)
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LOCATION: (222529)...(223869)
OTHER INPORMATION: unisc feature
LOCATION: (222529)...(22869)
OTHER INPORMA
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US-09-198-452A-1/c

US-09-198-452A-1/c

Sequence 1, Application US/09198452A

Sequence 1, Application US/09198452A

Sequence 1, Application US/09198452A

Sequence 1, Application US/09198452A

GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preversity RPHICATION NUMBER: US/09/198,452A

GURRENT RPILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849
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                                                                                                                                                                                                                                                                                                                                  Gaps
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APPLICANT: WATAMBE, HIDEMI
APPLICANT: WATAMBE, HIDEMI
APPLICANT: WATAMBE, HIDEMI
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILLE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT PILING DATE: 2001-02-23
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SEQ ID NOS: 7
LENGTH: 640681
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                                                                                                                                                                                                                                                                          Query Match 1.7%; Score 20; DB 4; Length 392000; Best Local Similarity 100.0%; Pred. No. 6.8; Matches 20; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.7%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 6.7
Matches 20; Conservative 0; Mismatches
NAME/KEY: exon:intron junction
| LOCATION: [148578]...(348579]
| CTHER INFORMATION: exon 10:intron 10
| NAME/KEY: intron
| LOCATION: (148579)...(3181838)
| CTHER INFORMATION: intron 10
| NAME/KEY: intron:exon junction
| LOCATION: (386185)...(386186)
| COCATION: (386185)...(386186)
| US-10-027-983-11
                                                                                                                                                                                                                                                                                                                                                                                                                              276309 AATAAATGAAAGAAAAAG 276290
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LOCATION: (1).7(15000)
OTHER INFORMATION: n=a or c or g or
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; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Buchnera Sp.
US-09-790-988-1
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LENGTH: 1230025
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us-10-015-637-1.oli.rni

LOCATION: (375001)...(390000)
OTHER INFORMATION: ma or c or g or t
NAME/KEX: misc feature
LOCATION: (390001)...(40000)
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NAME/KEX: misc feature
LOCATION: (435001)...(450000)
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NAME/KEX: misc feature
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NAME/KEX: misc feature
LOCATION: (610001)...(610000)
OTHER INFORMATION: ma or c or g or t
NAME/KEX: misc feature
LOCATION: (610001)...(610000)
OTHER INFORMATION: ma or c or g or t
NAME/K

107 AAATATAACACACACAAAA 125

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RESULT 14
US-09-134-01C-391/C

Sequence 391, Application US/09134001C

Sequence 391, Application US/09134001C

SEQUENCE 310, Application US/09134001C

GENERAL INFORMATION:

APPLICANT DOUGLET CAID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: DEDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DEPLEMENT US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 391

LENGTH: 1776
                                                                      US-09-489-039A-2871/c

Sequence 2871, Application US/09489039A

Sequence 2871, Application US/09489039A

Patent No. 651086

SEQUENCES INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489, 039A

CURRENT PAPLICATION NUMBER: US/09/489, 039A

CURRENT PAPLICATION NUMBER: US/09/489, 039A

PRIOR PILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

LENGTH: 1212
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Patent No. 6607879
GENERAL INPORMATION:
COCKS, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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1.7%; Score 19; DB 4; Length 1212;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 TTAATATATAATTGTAAT 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2871
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US-09-023-655-301
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ilarity 100.0%; Pred. No. 25;
Conservative 0; Mismatches 0; Indels
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NAME/KEY: misc feature
LOCATION: 1=a or c or g or c
NAME/KEY: misc feature
LOCATION: 1-a or c or g or c
NAME/KEY: misc feature
LOCATION: (755001)...(756000)
CTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (785001)...(785000)
CTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
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CTHER INFORMATION: n=a or c or g or t
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CTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
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US-09-669-751-213
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Best Local Similarity
Matches 19; Conserv
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ADDRESS: 1508
CORRESPONDENCE ADDRESS:
STREET: 3174 PORTER PRANACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
CONTRY: USA
CONFUTER: READABLE FORM:
MEDITUR TYPE: IA TO POPP dist.bl
COMPUTER: IBW PC COMPABLED!
SOFWARE: WORD PERCEC 6.1 FOR Windows/MS-DOS
SOFWARE: WORD Perfect 6.1 FOR Windows/MS-DOS 6.2
SOFWARE: WORD Perfect 6.1 FOR Windows/MS-DOS 6.2
SOFWARE: WORD Perfect 6.1 FOR Windows/MS-DOS 6.2
SOFWARE: WORD PERFETTION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE:
CLASSITCATION NUMBER: PA-001 US
FILING DATE:
ATTORNAYABET TINGRAMION:
NAME: Zeller, Karen J.
REGISTATION NUMBER: PA-001 US
TELECOMMUNICATION: INFORMATION:
NAME: CALSO BS-GS-GS-GS-STELENCE.CHARACTERISTICS:
INFORMATION FOR SEQ ID No: 301:
SEQUENCE CHARACTERISTICS:
LENGTH: 2590 base paire
TYPE: NUCLEIC exid
STRANDEDAES: single
TYPE: UNMEDIATE SOURCE:
LIBEATY: LATTITUO2
CLONE: 1133065
US-09-023-655-301
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Search completed: June 2, 2004, 07:16:20 Job time : 117 secs

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0; Gaps

Query Match
Best Eocal Similarity 100.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels

EX693278 BX693278 CG7765596 PC51-129 CG775596 PC51-1-29 R58612 EXP3012 BT93019 A380112 EST93059 CE378526 rg118-12.9 AL478092 T brucei CE223942 tigr-qss-CE323942 tigr-qss-CE323942 tigr-qss-CE323942 tigr-qss-CE323942 tigr-qss-CE323942 tigr-qss-CE323943 rud2c05.y CC586297 CH240-383 BZ.63794 CH230-339 AL551282 tg23h07.x T1440 SMEST0101 S AA528923 NAAD0160. AA528589 MAAD0153. CD072757 MA2-00527 AW017393 EST272815 AA801591 SWEST22815 AA508323 MAAD0415. AA508323 MAAD0415. AB137469 EST272815 BH339146 BOHHG527F

Sequence:

Title:

Run on:

Searched:

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BH570165 846 bp DNA linear GSS 14-DEC-2001
BCGPE54TR BOGP Brassica oleracea genomic clone BOGPE54, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brassica oleracea
Brassica oleracea
Brassica blantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
Town, C.D., Van Ake6,
Whole genome shotgun sequencing of Brassica oleracea
Other GSSs: BOGPES4TF
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523
Fax: 301-838-0208
Email: cdcown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn. Seg primer: TR
Class: sheared ends.
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                                                                    AA380112
CB53856
TB18526
TB1852842
CB53643
CC5865043
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CC5865043
AA518923
AA518923
AA518923
AA51393
AA617393
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CA905893
CD190460
BZ882476
BX693278
CC474046
CG755596
R95629
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AI976918
AW017201
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                                                                                                              survey sequence.
BHS70165
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   VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
BH570165/c
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AUTHORS
TITLE
JOURNAL
COMMENT
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CE710533 tigr-gss-
BX122318 Danio rer
BX734218 BX734218
                                                                                                  June 2, 2004, 02:36:30 ; Search time 3383 Seconds (without alignments) 10133.545 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 taggatccttcaatagaaaa......agagagtgatggttaatgca 1148
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                                                                                                                                                                                                                                                                                                                  55026578
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                           27513289 segs, 14931090276 residues
                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                           summaries
                                                                          - nucleic search, using sw model
                                                                                                                                                                                                                 OLIGO_NUC
Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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gb_htc:*
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BH570165 CE710533 BX122318 BX734218

846 194 491 536

2242

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Result No.

R55404 SMNHADA0090 CD171263 MS1-0010T R95607 SMNHADA0170 A1976293 EST270887 CA905893 PSC64291 CD190460 MS1-0064U ANOT7025 EST272480 A1076918 EST278480 A1076918 EST278480

AAS28868 MAAD307.
A1977349 EST271943
R55403 SMNHADA0000
R95405 SMNHADA0090
A1976001 EST270595
A1977237 EST271831

Wed Jun

FEATURES

ORIGIN

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AUTHORS
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BX734218
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The Institute for Genomic Research
Department of Endaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0206
Fax: 301-838-0208
Email: ekirknes@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS 29-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 194)
1 (kriness, E.P., Bafna, V., Halpern, A.L., Eevy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                    194 bp DNA linear GSS 29-SEP-20
tigr-gss-dog-17000369461433 Dog Library Canis familiaris genomic,
genomic survey sequence.
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                                                                                          /db_xref="taxon:3712"
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/clone=lib="BOGPE54"
/clone=lib="BOGPE54"
/clone="bocker: pdos: Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
                                                                                                                                                                                                                                                                   Gaps
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/mol type="genomic DNA"

/mol type="genomic DNA"

/strāin="Standard Poodle"

/db xref="raxon:9615"

/clone lib="Dog Library"

/note="Site 1: BetXI; Libraries were prepared from peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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Pred. No. 3.4;
                                                                                                                                                                                                                                                                   0; Indels
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                        1. .846
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/strain="TO1000DH3"
                                                                                                                                                                                                                           Query Match 2.2%; Score 25; DB Best Local Similarity 100.0%; Pred. No. 3.4 Matches 25; Conservative 0; Mismatches
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    Location/Qualifiers
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Canis familiaris
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TITLE JOURNAL MEDLINE PUBMED COMMENT

FEATURES

Matches

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REFERENCE AUTHORS

DEFINITION

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ACCESSION

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Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries:
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries:
This sequence was generated from the T7 end of BAC 72P11. 72P11 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
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BX734218 XGC-tadpole Silurana tropicalis cDNA clone TTpA076k17 5', mRNA sequence.
BX734218
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Hinxton, Cambridgeshire,
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
FROPICALIS SEQUENCE ID: TTPA076k17.plkSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
constructed by Nigel Garrett.
constructed by Nigel Garrett.
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construct
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Silurana tropicalis
Silurana tropicalis
Silurana tropicalis
Silurana tropicalis
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Silurana.

1 (bases 1 to 536)
Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
Sangar Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
Contact: Croning MDR
Danio rerio (zebrafish)
Danio rerio
Bubanio rerio
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes: Cyprinidae, Danio.

( Dases 1 to 491)
Humphray, S. J., Huckle, B. and Durham, J. L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Indels

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0; Mismatches
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                                       382 ATAACACACACAAAAATACATCTA 405
                                                                 351 ATAACACACAAAAATACATCTA 374
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    24; Conservative
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BX693278/c
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Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by AgResearch Ltd., New Zealand and The
      /clone="TTPA076k17"
/dev stage="tadpole (stage 35-40)"
/dev stage="tadpole (stage 35-40)"
/lab_host="coil pullub...
/clone lib="XG-ctadpole"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dT primed from Sig of poly A+ RNA from tadpole was oligo dT primed from Sig of poly A+ RNA from tadpole was bryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (cow)
Bos taurus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell type="Blood"
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/note="Vector: pARBAGL.3; Site 1: Mbol; Site_2: Mbol;
/note="Vector: pARBAGL.3; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
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Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvattsbeyn, A., Gebregeorgis, E., Chen, D., Riggs, F., de Crawford, A.M. and McEwan, J.C.
Bovine BAC End Sequences from Library CHORI-240
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 28; Length 696;
9.9;
                                                                                                                                                                                          DB 13; Length 536;
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0200
                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                   2.1%; Score 24; DB 100.0%; Pred. No. 10; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="breed: Hereford"
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Pred. No.
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/organism="Bos taurus"
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Seg primer: T7
Class: BAC ends.
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Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
BZ882476
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CC474046 820 bp DNA linear GSS 16-JUN-2003 CH240 298D10.TARBAC13P2 CHCRI-240 Bos taurus genomic clone CH240 298D10, genomic survey sequence. CC474046 CC474046.1 GI:31751163
733 bp mRNA linear EST 14-NOV-2003

EX693278 XGC-neurula Silurana tropicalis cDNA clone TNeu103f10 3',

EX693278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCSIO7; Site 1: EcoR1; Site 2: Not1; cDNA was oligo dT primed from Sug of poly A+ RNA from neurula. EcoR1-Not1 cut cDNA was then ligated into pCSIO7 with EcoR1 at the 5' end and Not1 at the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus
Bos taurus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                              Silurana tropicalis (western clawed frog)
Silurana tropicalis
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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100.0%; Pred. No. 9.8;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/clone lib="XGC-neurula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Silurana tropicalis"
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/clone="TNeu103f10"
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12884007
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DEFINITION
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R95629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                                                                        The British Columbia Cancer Agency Genome Science Centre 600 W. 10th Ave. Vancouver, British Columbia, Canada V5Z 4E6 Tel: 604-877-6085
Fax: 604-877-6085
Fax: 604-877-6085
Fax: 604-877-6276
Email: rholtadogsc.ac
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejongemail.cho.org).
Clones may be purchaded from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the Blates -298 row: D column: 10
Seg primer: SP6
Class: BAC ends.
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoldea, Bovidae, Bovidae, Bovidae, Bos.

1 (bases 1 to 820)

1 (bases 1 to 820)

1 Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,

Tasi, M., Cloutier, A., Lee, D., Girn, M., Mayo, M.,

Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, R.,

Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,

Schein, J., Marram, M., de Jong, P., McMilliam, S., Barris, W.,

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398

Other GSSS: CH203

Other GSSS: CH203

Other GSSS: CH203
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Strinvasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Burtjer, J., van der Meulen, M. and Sommer, R. J.
An integrated physical and genetic map of the nematode Pristionchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1509 bp DNA linear GSS 24-OCT-2003
P051-1-F07.ya Ppa BcoRI BAC Library Pristionchus pacificus genomic,
Poperent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell type="Blood"
/cell type="Blood"
/clone lib="CHOR1-240"
/note="Vector: pTARBACL.3; Site 1: Wbol; Site 2: Mbol;
Hereford bull il Domino 99375; CHOR1-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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Mol. Genet. Genomics 269 (5), 715-722 (2003)
22835951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="breed: Hereford"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    forganism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9913"
/clone="CH240_298D10"
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                                                                                                                                                                                                                                                                                                                                                Sequencing
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/GIGILENS-SOLITE CONTROLLS (ADDITION CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS CONTROLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="california"
/db xref="taxon:54126"
/clone_lib="Ppa BCORI BAC Library"
/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schistosoma mansoni
Bukaryota; Metazoa: Platyhelminthes; Trematoda; Digenea;
Strigeldida; Schistosomatoidea; Schistosoma.
1 (bases 1 to 259)
Ridgers,I.L.
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Unpublished (1995)
Contact: Ridgers, I.L.
Experimental Taxonomy Unit, Zoology
The Natural History Museum
Crowwell Road, South Kensington, London, SW7 5BD, U.K.
Tel: 01719389297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 29; Length 1509;
Pred. No. 8.4;
0; Mismatches 0; Indels
                                    Bvolutionary Biology
Max-Phanck-Institute for Developmental Biology
Max-Phanck-Institute for Developmental Biology
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pristionchus pacificus"
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                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Contact: Sommer RJ
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Seg primer: SK.
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Eukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

(CE (bases 1 to 307)

Rammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(CE)

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,

Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,

White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,

Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,

Fitzgerald,L.M., Fitzhugh,M.M., Fritchman,J.L., Geoghagen,N.S.,

Glodek,A., Ghehn,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,

Kelley,J.M., Kalley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,

Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,

Phillips,C.A., Spriggs,T.A., Utterbock,T.R., Weidman,J.F., Li,Y.,

Bednarik,D.P., Feng, T.A., Collemn,T.A., Collins,B.J.,

Dinke,D., Feng, Cao,L., Cepeda,M.A., Colemn,T.A., Collins,B.J.,

Kozak,D.L., Kunsch,C., Hungjun,J., Hatsings,G.A., Mix,M.K.,

Raymond,L., Well,Y.F., Wing,J., Xu,C., Yu,G.L., Raben,S.M.,

Praser,C.M. and Vence,J.J.C.

Initial assessment of human gene diversity and expression patterns

based upon 33 million mucledides of cDNA sequence
genes). The size range of inserts for the library was 0.5Kb - 2.5 Kb, the cDNA being directionally cloned between the EcoxI and the KhoI sites of the Bluescript phagemid was excised by mass in vivo excision of the library and inserted into E coli XLI Blue. The plasmid was purified using the Giagen Giavel B system and sequenced with Tag dye-terminator chemistry (SK,T3 and T7 primers) for ABI 373A. The library was prepared by Hanan Abdel Ramed, Ain Shams Univ., Cairo and provided by Kohamed Saber, Theodore Bilharz Research Institute,
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For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
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EST93059 Skin tumor I Homo sapiens cDNA 5' end, mRNA sequence
AA380112
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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Contact: Kerlavage, AR
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Heterodera glycines

Heterodera glycines

Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;

Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.

Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.

Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.

Tobases 1 to 449)

RS Mylie; T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Wylie; T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Wylie; T., Dante, M., Riters, E., Bennett, J., Franklin, C., Bowers, Y., Gibbons, M., Allen, M., Person, B., Swaller, T.,

Tragareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Gardenas, M., McCann, R., Waterston, R., and Wilson, R., Toleckon, Y., Cardenas, M., Harvey, M., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Harvey, M., Schurk, R., Nohn, S., Shin, T., Jackson, Y., Cardenas, M., The Washington Univ. Nematode EST Project, 1999

AL Unpublished (1999)

AL Unpublished (1999)

At Harvey, M., Schurk, School of Medicine
4444 Forest park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810

Fax: 314 286 1810

Frax: 314 286 1810

Frax: 314 286 1810

This library was generated by cloning cDNAs directionally into
This library was generated by cloning cDNAs directionally into
Uni-Zapy(strategene) (T3 primer/EcoRI are at the 5'-end and T7/KhoI
are at the 3'-end: The library was excited [now in pallescript
SKI+)] and normalized (Bonado et al 1996 Genome Research

Iowa State University, Plant Pathology Department and Jeff
McDermott (jpmcderm@iastate.edu).

Putative full length read
The vector Inergah is 479
Seq primer: T3 from Gibco
High quality sequence stop: 449.

High quality sequence stop: 449.
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/nore="Organ: skin; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
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/mol_type="mRNA"
/db_xref="taxon:51029"
                                                                                                                                                                                                                                                                                                                             DB 9;
32;
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Query Match

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Confect: Kirkness &F
Confect: Kirkness &F
Confect: Kirkness &F
Confect: Maryotic Genomic Research
Department of Bukaryotic Genomics, TiGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Rockville, MD 388-0208
Pax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CE222942 611 bp DNA linear GSS 25-SEP-2003 tigr-gss-dog-17000326866999 Dog Library Canis familiaris genomic, genomic survey sequence.
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He Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
El: 301-838-0200
Pax: 301-838-0200
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Canis familiaris
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Canis familiaris
Enkaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota, Butheria; Carnivora; Fissipedia; Canidae; Canis.
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                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.

    (bases 1 to 604)

                                                                                                                                                    Kirkness, B.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone libe."Dog Library"
//note="Site_1: Betx1; Libraries were prepared from
peripheral blood"
                                                                                                                                                                                                                                                                    The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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/db_xref="taxon:9615"
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                Canis familiaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14512627
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                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
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                                                                                                                                                                                                                                                                    TITLE
JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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COMMENT
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PUBMED
COMMENT
                                                                                                                       REFERENCE
                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A, E-mail: barrell@sanger.ac.uk and nhlosanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),
Rockwille, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU327/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kD). The v + i method used for the library construction is described in detail in Smith, H. and Wenter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing projects. In Genome Sequencing Projects. In Genome Sequencing Projects. In Barris, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           543 bp DNA linear GSS 13-DEC-2000 T. brucel sheared genomic DNA clone 191e02, forward sequence, bidance.
lows State University, Plant Pathology Department and Jeff McDermott (jpmcderm@iastate.edu)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        604 bp DNA linear GSS 29-SEP-204 Ligr-gss-dog-17000312937745 Dog Library Canis familiaris genomic, PRADARCO Survey sequence.
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Trypanosoma bruces
Bukaryota; Daglenosoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                    2.0%; Score 23; DB 14; Length 449;
100.0%; Pred. No. 30;
iive 0; Mismatches 0; IndelB
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100.0%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08; Pred. no.
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/strain="TREU927"
/db_xref="taxon:5691"
                                                                                                                                                                                                                                                                                                                                                      399 AACAAAACAAATTTATGTTTCAT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  635 AATATATATATATACAATTA 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 AATATATATATATATACAATTA 223
                                                                                                                                                                                                                                                                                                         60 AACAAACAAATTTATGTTTCAT 82
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                                                                                                                                                                                                                                   23; Conservative
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                                                                                                                                                                                             Local Similarity
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Canis familiaris (dog)

LOCUS DEFINITION

RESULT 13

CE607569

ACCESSION

VERSION KEYWORDS SOURCE

Query Match Best Local

ORIGIN

FEATURES

Matches

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0; Gaps

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Sequence 391, Application US/09134001C

Radent No. 6380370

GRAERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR FULLOR DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/065,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: S674

SEQ ID NOS: S674
                                                                                                                                                                                                                 APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TILLE OF INVENTION: PREDMANIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERRANCE: 2709-2004001
CURRENT PELLING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
SEQ ID NOS: 14342
SEQ ID NOS: 14342
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Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.7%; Score 19; DB 4; Best Local Similarity 100.0%; Pred. No. 23; Matches 19; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 23,
Matches 19; Conservative 0; Mismatches
                                                                              RESULT 13
US-09-489-039A-2871/c
US-09-489-039A-2871, Application US/09489039A
Sequence 2871, Application US/09489039A
Parent No. 6610836
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 TIAATATAATAATTGTAAT 192
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107 AAATATAACACACAAAA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-134-001C-391/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-489-039A-2871
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US-09-023-655-301
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APPLICANT: Greenspan, Ralph J.
APPLICANT: Greenspan, Ralph J.
APPLICANT: Greenspan, Methods for Identifying Compounds for ITILIS OF INVENTION: Methods for ITILIS OF INVENTION: Methods for ITILIS OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to ITILIS OF INVENTION: Malance and the Perception of Gravity FILIS OF INVENTION NUMBER: US/09/669,751
CURRENT APPLICATION NUMBER: US 60/168,579
PRIOR PILING DATE: 1999-12-02
NUMBER OF SEQ ID NOS: 261
SOFTWARE: FRAISEQ for Windows Version 4.0
SEQ ID NO 213
LENGTH: 181
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1.7%; Score 19; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 19; Conservative 0; Mismatches 0; Indels
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6.5;
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                              NAME/KEY: misc_feature
LOCATION: (750001). (765000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (765001). (780000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (780001). (795000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (780001). (825000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (810001). (825000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (810001). (810000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (810001). (810000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (810001). (810000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (810001). (810000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (810001). (810000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (810001). (810000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (810001). (810000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (810001). (810000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
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               OTHER INFORMATION: n=a or c or g or
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US-09-669-751-213
; Sequence 213, Application US/09669751
; Patent No. 6551575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 GAAGAAAAAAGATTAAAAAA 122
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ORGANISM: Drosophila
US-09-669-751-213
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378 AAATATAACACACAAAA 396

us-10-015-637-1.oli.rni

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Query Match 1.7%; Score 19; DB 4; Length 2590; Best Local Similarity 100.0%; Pred. No. 23; Matches 19; Conservative 0; Mismatches 0; Indels
NUMBER OF SEQUENCES: 1508

CORRESPONDENCE ADDRESS:
ADDRESSEE: INCTTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO ALTO
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTY: PALO ALTO
STATE: CALIFORNIA
COUNTY: 18M PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: BEADABLE FORM:
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SOFTWARE: WOR PERFECT 6.1 for Windows/MS-DOS 6.2
CORRESPICATION: DATA:
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Search completed: June 2, 2004, 07:16:20 Job time: 117 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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2, 2004, 02:24:29; Search time 537 Seconds (without alignments) 9081.809 Million cell updates/sec

US-10-015-637-1 1148 Perfect score:

1 taggatccttcaatagaaaa.......agagagtgatggttaatgca 1148 Scoring table: Seguence:

OLIGO\_NUC Gapop\_60.0 , Gapext 60.0

3373863 seqs, 2124099041 residues Searched:

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Post-processing: Listing first 45 summaries

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Pred. No. is the mumber of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description		Abn83929 Arcelin-5	-	Aad29066 Phaseolus	Abn83928 Arcelin-4	Abn83927 Arcelin-3	-			Abn83924 Arcelin-3	Aan90025 DNA encod	Abz80122 Arcelin 5	Aas62538 cDNA sequ	Aba46475 Human bre	Aak30701 Human bon		Add48876 Human gen		Abl21668 Drosophil	Abk40036 Human che	Abl70602 Chemicall	Aaa95933 Human KLK	Aak87515 Human imm
	TD	ABN83916	ABN83929	ABN83917	AAD29066	ABN83928	ABN83927	ABN83926	AAQ94051	ABN83925	ABN83924	AAN90025	ABZ80122	AAS62538	ABA46475	AAK30701	AAK05134	ADD48876	AAS43419	ABL21668	ABK40036	ABL70602	AAA95933	AAK87515
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## ALIGNMENTS

BP. ABN83916 standard; DNA; 1148 RESULT 1 ABN83916

(first entry)

06-SEP-2002

Truncated P. vulgaris exotic genotype G02771 Arcelin-5 promoter sequence.

Arcelin-5; promoter; plant; transgenic; soybean; agriculture; nutrition; pharmaceutical; ds.

Phaseolus vulgaris.

WO200250295-A2.

27-JUN-2002. 

17-DEC-2001; 2001WO-US047495. 18-DEC-2000; 2000US-0255879P.

(RENE-) RENESSEN LLC

Oulmassov T; Dubois P, Liang J, Wang Q,

WPI; 2002-508809/54.

New transformed or transgenic soybeans plants or cells with an Arcelin-5 promoter, for use as an improved distary source of protein for humans or animals, or for producing soybeans with important agricultural or nutritional properties.

Claim 4; Page 65-66; 74pp; English.

The invention relates to a transformed soybean plant cell and transgenic soybean plant, both of which has a nucleic acid molecule comprising the phaseolus vulgaris exotic genotype 002771 Arcelin-5 promoter sequence. The transformed soybean plant cell and transgenic soybean plant are useful as an improved source of dietary protein for humans and livestock. These are also useful for producing soybean plants that exhibit important sequence represents the truncated producing soybean plants that exhibit important sequence represents the truncated p. vulgaris excit genotype 002771 Arcelin-5 promoter sequence. This sequence is a deletion mutant of the Arcelin-5 promoter, created by the removal of approximately 600 base

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pharmaceutical; ds.
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Matches 1148; Conservative 0; Mismatches 0; Indels 0;
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The invention relates to a transformed soybean plant cell and transgenic soybean plant, both of which has a nucleic acid molecule comprising the phase-clus vulgaris exotic genotype 02271 Arcelin-5 promoter sequence. The transformed soybean plant cell and transgenic soybean plant are useful as an improved source of dietary protein for humans and livestock. These are also useful for producing soybean plants that exhibit important agricultural, nutritional or pharmaceutical properties. The current sequence represents a truncated P. vulgaris exotic genotype 602771 Arcelin-5 promoter sequence. This sequence was used in the expression of a GUS reporter gene in a soybean cotyledon
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                                                                                                                                                                                                                                                                                                                                                        New transformed or transgenic soybeans plants or cells with an Arcelin-5 proneter. for use as an improved dietary source of protein for humans or animals, or for producing soybeans with important agricultural or nutritional properties.
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                                                                               Arcelin-5; promoter; plant; transgenic; soybean; agriculture; nutrition; pharmaceutical; ds.
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                                                      P. vulgaris exotic genotype G02771 Arcelin-5 promoter #2
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The invention relates to heterologous gene expression in plants. The invention also relates to seed preferred expression cassette having gene regulatory elements comprising arcelin promoter, arcelin 51 leader, and arcelin 513' end. This expression cassette is useful for heterologous gene expression in plants. The protein encoded by the heterologous gene is a slingle chain antibody variable fragment (scPv). The present sequence is Phaseolus vulgaris arcelin promoter of the invention

Seguence 1821 BP; 698 A; 308 C; 210 G; 605 T; 0 U; 0 Other;

Novel seed preferred expression cassette having gene regulatory elements comprising arcelin promoter, arcelin 51 leader, and arcelin 51 3' end, useful for heterologous gene expression in plants.

Claim 1; Page 46-47; 52pp; English.

Depicker A

Goossens A,

De Jaeger G,

Angenon G,

WPI; 2002-139925/18.

(VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG

31-MAY-2001; 2001WO-EP006298.

03-JAN-2002

29-JUN-2000; 2000EP-00202278

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 Score 1046; DB 6;
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0; Mismatches 2;
Query Match
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Heterologous gene expression; plant, arcelin promoter; arcelin leader; seed preferred expression cassette; ds.

Phaseolus vulgaris

Phaseolus vulgaris arcelin promoter.

07-MAY-2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arcelin-4 full length promoter sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    ABN83928 standard; DNA; 1866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-508809/54
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humans or
or
                                                                                                         The invention relates to a transformed soybean plant cell and transgenic soybean plant, both of which has a nucleic acid molecule comprising the phaseolus vulgaris excitic genotype 602/71 Arcelin-5 promoter sequence. The transformed soybean plant cell and transgenic soybean plant are useful as an improved source of dietary protein for humans and livestock. These are also useful for producing soybean plants that exhibit important agricultural, nutritional or pharmaceutical properties. The gurrent sequence represents an arcelin-4 full length promoter sequence
                                                                                                                                                                                                                                                                                                                                                                                       921
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pharmaceutical; ds.
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 humans
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promoter, for use as an improved dietary source of protein for animals, or for producing soybeans with important agricultural nutritional properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGCACTCCTCTCACTTCCCATTGCTACCTACCAAACCGCTTCTCTC 1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCACTCCTCTCACTTCCCATTGCTACCTGCCAAACCGCTTCTCTC 968
                                                                                                                                                                                                                                                                                                                 Length 1866;
                                                                                                                                                                                                                                                                              Sequence 1866 BP; 692 A; 339 C; 209 G; 626 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                               9.3%; Score 107; DB 6; I
100.0%; Pred. No. 1.8e-38;
tive 0; Mismatches 0;
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                                                                            Example 1; Fig 4; 74pp; English
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Matches 107; Conservative
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264 AGALTITGCALTIGITION 288
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Matches
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                                                                                                       862 TGCCACCTCAGCTCCCACCTCTCTCATTATGAGCCTACTGGCCATGCACACTGCCACCT 921
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sequence represents an arcelin-3 full length promoter sequence
                                                                                                                                                                       1604 CAGCACTCCTCTCACTTCCCATTGCTACCTGCCAAACCGCTTCTCTC 1650
                                                                                                                                                          968
                           Sequence 1872 BP; 694 A; 339 C; 209 G; 630 T; 0 U; 0 Other;
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100.0%; Pred. No. 2e-28;
ive 0; Mismatches 0; Indele
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                                                                             Indels
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                                                  Query Match 9.3%; Score 107; DB 6; L. Best Local Similarity 100.0%; Pred. No. 1.8e-38; Matches 107; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The DNA encodes a lectin-like protein isolated from kidney bean var. Kentucky Wonder. The gene provides insect-resistance to crop plants, is also useful as a DNA marker in gene and genomic analysis
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                                                                                                                                                          lectin-like; kidney bean; insect resistance; genomic analysis;
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Local Similarity 100.0%; Pred. No. 2e-08;
hes 41; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New kidney beam gene encoding lectin-like protein insect-resistant crop plants.
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AAQ94051 standard; DNA; 1211 BP
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                                                                                                                        Kidney bean lectin-like gene.
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                                                                                                                                                                                                                         Phaseolus vulgaris.
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                                                                                                                                                                                  DNA marker; ss.
                                                                                                                                                                                                                                                                                                                                           11-NOV-1993;
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                                                                               10-MAY-1996
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Best Local Similarity Matches 85; Conserv

1037 ICGITGTTTAATAAT

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204 TCGTTGTTTAATAATTGTTAATTTGGAGTTGAATAATAAAATGAAAGAAAAAGTTGGAA

1097 AGATTTTGCATTTGTTGTTGTATAA 1121

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2.3%; Score 26; DB 6; 100.0%; Pred. No. 0.14; ative 0; Mismatches

Length 322;

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useful as an improved source of dietary protein for humans and livestock. These are also useful for producing soybean plants that exhibit important agricultural, mutritional or pharmaceutical properties. The current sequence represents an arcelin-3 promoter sequence fragment
The transformed soybean plant cell and transgenic soybean plant are
                                                                        Sequence 322 BP; 114 A; 37 C; 38 G; 133 T; 0 U; 0 Other;
                                                                                                  Query Match
Best Local Similarity 100.0
Matches 26; Conservative
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                                                                                                                                                                           The invention relates to a transformed soybean plant cell and transgenic soybean plant, both of which has a nucleic acid molecule comprising the Phaseclus vulgaris exotic genotype 60271 Arcelin-5 promoter sequence. The transformed soybean plant cell and transgenic soybean plant are useful as an improved source of dietary protein for humans and livestock. These are also useful for producing soybean plants that exhibit important agricultural, nutritional or pharmaceutical properties. The current sequence represents an arcelin-4 promoter sequence fragment
                                                                                      New transformed or transgenic soybeans plants or cells with an Arcelin-5 promoter. for use as an improved dietary source of protein for humans or animals, or for producing soybeans with important agricultural or nutritional properties.
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                                     Oulmassov T;
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                                      Liang J,
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             (RENE-) RENESSEN LLC
                                                             WPI; 2002-508809/54
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                                     Dubois P,
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                                      Wang Q,
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                                                                                                                                                                                                                              DNA encoding antigenic circumsporozoite protein of Plasmodium malariae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigenic protein for vaccination against malaria - encoded by cloned gene coding for plasmodium malariae circumsporozoite protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 1; 11pp; English.
                      AAN90025 standard; DNA; 1542 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88US-00238746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89US-00238746.
                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
424. .1036
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) NAT INST OF HEALTH
                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        98. .1383
                                                                                                                               (revised)
                                                                                                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                          Plasmodium malariae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1989-172958/23.
                                                                                                                          25-MAR-2003
17-DEC-2001
01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USN7238746-N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-1989.
                                                                          AAN90025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
AAN90025/c
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634 GAATATATATATATATACAATTAA 658

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The invention relates to a transformed soybean plant cell and transgenic soybean plant, both of which has a nucleic acid molecule comprising the Phaseolus vulgaris exotic genotype G02771 Arcelin-5 promoter sequence.

1 CCACGTGAGCTCCTTCCTTCCC 24

RESULT 13

(first entry)

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Sequence 24 3P; 2 A; 12 C; 3 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                     Arcelin 5 promoter PCR primer SEQ ID NO:79.
1513 GAATATATATATATATACAATTAA 1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 94; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MONS ) MONSANTO TECHNOLOGY LLC.
                                                                                                                                                                                  ABZ80122 standard; DNA; 24 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-AUG-2002; 2002WO-US026047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L7-AUG-2001; 2001US-0312758P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-268314/26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003016482-A2
                                                                                                                                                                                                                                                                                                       22-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Levering C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                ABZ80122;
                                                                                                                    RESULT 12
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Valentin HE, Karunanandaa B,

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The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polymucleotide sequences. The proteins are useful for identifying compounds that modulate their compounds that modulate expression of the polymucleotide sequences. Or compounds that modulate expression of the polymucleotide sequences encoding the secreted proteins. The sequences of the invention are useful immune deficiency disorders (e.g. severe combined immunodeficiency (SCID), autoimmune disorders (e.g. severe combined immunodeficiency (SCID), autoimmune disorders (e.g. multiple selerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis). The polymucleotide sequences of the invention are also useful in gene therapy. AAS62214-AAS6238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Resnick RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding secreted proteins useful for treating
                                                                                                                                                                                                                            Human secreted protein; hyperproliferative disorder; autoimmune dis
immune deficiency disorder; blood disorder; inflammatory disorder;
infectious disorder; gene therapy; antimicrobial; hepatotropic;
immunosuppressive; antirheumatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1224 BP; 395 A; 205 C; 204 G; 420 T; 0 U; 0 Other;
                                                                                                                                                                             cDNA sequence #325 encoding novel human secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Howes SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24; DB 6;
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Scc...
v 100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          763 TITAAAAATATAATITITAAAAA 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501 TTTAAAAATATATTTTAAAAA 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 246; 391pp; English.
                         AAS62538 standard; cDNA; 1224 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fechtel K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides encoding secasthma, HIV and Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABA46475 standard; DNA; 400 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAR-2001; 2001WO-US010485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2000; 2000US-0195604P.
                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wong GG, Clark HF, Fe
Gulukota K, Graham JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI, 2002-010900/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                    WO200177291-A2
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                          14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
                                                                           AAS62538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        datches
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ABA46475/c
AAS62538/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AXX
                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a substantially purified tocopherol protein (1). Also described is a method (M) for reducing expression of methyltransferase 1 (MT1) or gamma-tocopherol methyltransferase (GMT) in a plant, by transforming a plant with a nucleic acid molecule having an exogenous promoter region which functions in plant cells to cause the production of an mRNA molecule, and growing the transformed plant. (M) is useful for increasing the gamma-tocopherol content. A polymucleotide (II) encoding (I) can be used for producing a plant having a seed with an increased alpha-tocopherol or alpha-tocorimon level. (II) is useful for increased alpha-tocopherol or alpha-tocorimon level. (II) is useful for increased alpha-tocopherol or alpha-tocorimon level. (II) is useful for obtaining the reduction of the expression, expression, overexpression of (I) in a transformed plant to provide tolerance to a variety of stress, cold tolerance such as to expens to a cone, UV tolerance, or fungal/microbial pathogen tolerance. (II) is useful for obtaining other nucleic acid molecules or homologues from the same species, to screen cDMA or genomic libraries, to isolated promoters of cell enhanced, cell specific, tissue enhanced, tissue specific, developmentally or environmentally regulated expression profiles, as markers, for detecting single nucleotide polymorphisms, and to determine the level of (I) in a plant or pattern of expression of (I) encoded in pare an arcelin 5 promoter sequence represents a PCR primer for an arcelin 5 promoter sequence, which is used in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel substantially purified tocopherol protein and nucleic acid encoding the same, useful for producing a plant having a seed with increased alpha
                                                                                                                                                                                                                                                           Gamma-tocopherol methyltransferase; methyltransferase; tocopherol; alpha-tocoritenol; siress; oxidative stress tolerance; oxygen; ozone; UV tolerance; ultra violet tolerance; cold tolerance; tungal pathogen; microbial pathogen; plant; enzyme; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hao M, Aasen E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Gaps

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                          Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma; ss.
            Human bone marrow expressed single exon probe SEQ ID NO: 5258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; SEQ ID NO 5258; 658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000668
                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488900/53
                                                                                                                                40200157276-A2.
                                                                                                                                                                                                                                                                                                                   27-SEP-2000;
04-OCT-2000;
                                                                                                  Homo sapiens
                                                                                                                                                                                                                                     04-FEB-2000;
                                                                                                                                                                                                                                                     26-MAY-2000;
                                                                                                                                                                                                                                                                                     03-AUG-2000;
                                                                                                                                                                                                                                                                                                     21-SEP-2000;
                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                       Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and Br 474 cells. The method involves contacting the probes with a collection of detectably labelled mucleic acids derived from mRNA of human breast, and then measuring the label bound to each probes of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring this invention presents as bus than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the present sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                  Human; microarray; single exon probe; gene expression; breast; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                claim 1; SEQ ID NO 5170; 327pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
2.0%; Score 23; DB 4; Length 400;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 400 BP; 89 A; 85 C; 94 G; 132 T; 0 U; 0 Other;
                                                   Human breast cell single exon nucleic acid probe #5170.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W, Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           490 AAATACAAATATTTAAAAAATAT 512
                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                       03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US000662
                                                                                                                                                                                                                                                                          2000US-0180312P
                                                                                                                                                                                                                                                                                        2000US-0207456P.
                       (first entry)
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Chen W, Rank DR,

2000US-00632366. 2000US-0234687P. 2000US-0236359P. 2000GB-00024263.

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                               2.0%; Score 23; DB 4; Length 400; 100.0%; Pred. No. 3.2; ative 0; Mismatches 0; Indels
Sequence 400 BP; 89 A; 85 C; 94 G; 132 T; 0 U; 0 Other;
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ne : 547 Becs
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                                 Query Match
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AAK30701 standard; DNA; 400

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ALIGNMENTS

PAT 15-JUL-2002 Phaseolus vulgaris Phaseolus vulgaris Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; linear DNA AX463281 1148 bp Sequence 1 from Patent WO0250295. AX463281 GI:21886232 AX463281.1 Phaseolus. RESULT 1
AX4632B1
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOUNCE
ORGANISM REFERENCE AUTHORS

1
Oulmassov,T., Wang,Q., Dubois,P. and Liang,J.

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1514 GACACCACTGGGCATGCATGCTGCCACCTCAGCTCCCACCTCTTCTCATTATGAGCCTAC 1573
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Submitted (01-AUG-1995) Goossens A., Universiteit Gent,
Laboratorium Genetika, K.L.Ledeganckstraat 35, Gent, Belgium, 9000
Revised by [4]
4 (bases 1 to 3900)
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Submitted (13-AUG-1998) Goossens A., Universiteit Gent,
Laboratorium Genetika, K.L.Ledeganckstraat 35, Gent, Belgium, 9000
On Aug 25, 1998 this sequence version replaced gi:929816.
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arc5-1 gene; arcelin 5a.
Phaseolus vulgaris
Phaseolus vulgaris
Phaseolus vulgaris
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Isolation and characterisation of arcelin-5 proteins and cDNAs
Bur. J. Biochem. 225 (3), 787-795 (1994)
95045555
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Nucleotide sequence of an arcelin5-I genomic clone from wild
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Plant Physiol. 109, 722-722 (1995)
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/mol_type="unassigned DNA"
/db xref="taxon:3885"
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